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Attention: Examiner \_\_\_\_\_, Art Unit 16xx \_\_\_\_\_

**PATENT**

Attorney Docket No.  
DX0724XK1

CN 028008

Date: September 10, 2001 By: Jeffrey Gillis  
Jeffrey Gillis

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of:

Gerard T. HARDIMAN, et al.

Serial No.: to be assigned

Filed: SEPTEMBER 10, 2001

For: HUMAN RECEPTOR PROTEINS;  
RELATED REAGENTS AND  
METHODS

Examiner: not assigned

Art Unit: not assigned

USE OF PRIOR SEQUENCE  
SUBMISSION UNDER 37 CFR §1.821(e)

Palo Alto, California 94304

SEPTEMBER 10, 2001

Assistant Commissioner for Patents  
Box: Patent Application  
Washington, D.C. 20231

Sir:

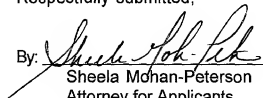
The attached copy of the Sequence Submission is for the patent application submitted herewith. The computer readable form in this application is equivalent to with that filed in parent application USSN 09/728,540. In accordance with 37 CFR 1.821(e), please use the computer readable form submitted in that application on July 17, 2001, as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for computer readable form that will be used for the instant application.

The attached copy of the Sequence Submission was originally submitted to the patent office in the parent application, USSN 09/728,540, in response to the Notice to Comply with Requirements for Patent Applications containing Nucleotide and/or Amino Acid Sequences dated June 7, 2001, for incorporation into the specification, on July 17, 2001.

Respectfully submitted,

Dated: September 10, 2001

By:

  
Sheela Mohan-Peterson  
Attorney for Applicants  
Reg. No. 41,201

DNAX Research Institute  
901 California Avenue  
Palo Alto, California 94304-1104  
Tel: (650) 496-6400  
Fax: (650) 496-1200

# SEQUENCE LISTING

<110> Hardiman, Gerard T.  
 Rock, Fernando L.  
 Bazan, J. Fernando  
 Kastelein, Robert A.  
 Ho, Stephen W.K.  
 Liu, Yong-Jun

<120> Human Receptor Proteins; Related Reagents and Methods

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Gln	Trp	Pro	Glu	Lys	Met	Lys	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Arg	Ile		
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His	Ser	Val	Thr	Gly	Cys	Ile	Pro	Lys	Thr	Leu	Glu	Ile	Leu	Asp	Val		
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470

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acg ttt tct aag gag caa ctt gac tca ttt cac aca ctg aag act ttg 1584  
Thr Phe Ser Lys Glu Gln Leu Asp Ser Phe His Thr Leu Lys Thr Leu  
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Glu Ala Gly Gly Asn Asn Phe Ile Cys Ser Cys Glu Phe Leu Ser Phe  
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700 705 710	

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Leu Asn Leu Leu Gly Asn Pro Tyr Lys Thr Leu Gly Glu Thr Ser Leu  
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 Phe Ser His Leu Thr Lys Leu Gln Ile Leu Arg Val Gly Asn Met Asp  
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 Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu  
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 Glu Cys Leu Glu Leu Arg Asp Thr Asp Leu Asp Thr Phe His Phe Ser  
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 Asp Pro Gly Lys Val Glu Thr Leu Thr Ile Arg Arg Leu His Ile Pro  
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 Arg Phe Tyr Leu Phe Tyr Asp Leu Ser Thr Leu Tyr Ser Leu Thr Glu  
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 315 320 325 330  
 Cys Leu Leu Ser Gln His Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser  
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 Ser Leu Glu Lys Thr Gly Glu Thr Leu Leu Thr Leu Lys Asn Leu Thr  
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His	Ser	Val	Thr	Gly	Cys	Ile	Pro	Lys	Thr	Leu	Glu	Ile	Leu	Asp	Val
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Cys	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp
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Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu
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Glu	Asn	Phe	Val	Lys	Ser	Glu	Trp	Cys	Lys	Tyr	Glu	Leu	Asp	Phe	Ser
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Leu	Glu	Pro	Ile	Glu	Lys	Lys	Ala	Ile	Pro	Gln	Arg	Phe	Cys	Lys	Leu
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Arg	Lys	Ile	Met	Asn	Thr	Lys	Thr	Tyr	Leu	Glu	Trp	Pro	Met	Asp	Glu
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Homo sapiens

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Glu	Val	Ala	Asp	Cys	Ser	His	Leu	Lys	Leu	Thr	Gln	Val	Pro	Asp	Asp	
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Leu	Pro	Thr	Asn	Ile	Thr	Val	Leu	Asn	Leu	Thr	His	Asn	Gln	Leu	Arg	
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Lys	Leu	Pro	Met	Leu	Lys	Val	Leu	Asn	Leu	Gln	His	Asn	Glu	Leu	Ser	
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Gln	Leu	Ser	Asp	Lys	Thr	Phe	Ala	Phe	Cys	Thr	Asn	Leu	Thr	Glu	Leu	
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Leu	Leu	Ser	Asn	Asn	Lys	Ile	Gln	Ala	Leu	Lys	Ser	Glu	Glu	Leu	Asp	
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Trp	Thr	Asn	Leu	Thr	Met	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	Asn	Val	
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[illegible]

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Leu	Leu	Ile	His	Phe	Glu	Gly	Trp	Arg	Ile	Ser	Phe	Tyr	Trp	Asn	Val	
700					705				710						715	
tca	gta	cat	cga	gtt	ctt	ggg	ttc	aaa	gaa	ata	gac	aga	cag	aca	gaa	2256
Ser	Val	His	Arg	Val	Leu	Gly	Phe	Lys	Glu	Ile	Asp	Arg	Gln	Thr	Glu	
				720					725						730	
cag	ttt	gaa	tat	gca	gca	tat	ata	att	cat	gcc	tat	aaa	gat	aag	gat	2304
Gln	Phe	Glu	Tyr	Ala	Ala	Tyr	Ile	Ile	His	Ala	Tyr	Lys	Asp	Lys	Asp	
			735					740							745	
tgg	gtc	tgg	gaa	cat	ttc	tct	tca	atg	gaa	aag	gaa	gac	caa	tct	ctc	2352
Trp	Val	Trp	Glu	His	Phe	Ser	Ser	Met	Glu	Lys	Glu	Asp	Gln	Ser	Leu	
			750				755						760			
aaa	ttt	tgt	ctg	gaa	gaa	agg	gac	ttt	gag	gcg	ggg	gtt	ttt	gaa	cta	2400
Lys	Phe	Cys	Leu	Glu	Glu	Arg	Asp	Phe	Glu	Ala	Gly	Val	Phe	Glu	Leu	
	765					770					775					
gaa	gca	att	gtt	aac	agc	atc	aaa	aga	agc	aga	aaa	att	att	ttt	gtt	2448
Gln	Ala	Ile	Val	Asn	Ser	Ile	Lys	Arg	Ser	Arg	Lys	Ile	Ile	Phe	Val	
780					785					790					795	
ata	aca	cac	cat	cta	tta	aaa	gac	cca	tta	tgc	aaa	aga	ttc	aag	gta	2496
Ile	Thr	His	His	Leu	Leu	Lys	Asp	Pro	Leu	Cys	Lys	Arg	Phe	Lys	Val	
				800				805						810		
cat	cat	gca	gtt	caa	caa	gct	att	gaa	caa	aat	ctg	gat	tcc	att	ata	2544
His	His	Ala	Val	Gln	Gln	Ala	Ile	Glu	Gln	Asn	Leu	Asp	Ser	Ile	Ile	
			815					820					825			
ttg	gtt	ttc	ctt	gag	gag	att	cca	gat	tat	aaa	ctg	aac	cat	gca	ctc	2592
Leu	Val	Phe	Leu	Glu	Glu	Ile	Pro	Asp	Tyr	Lys	Leu	Asn	His	Ala	Leu	
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tgt	ttg	cga	aga	gga	atg	ttt	aaa	tct	cac	tgc	atc	ttg	aac	tgg	cca	2640
Cys	Leu	Arg	Arg	Gly	Met	Phe	Lys	Ser	His	Cys	Ile	Leu	Asn	Trp	Pro	
	845					850					855					
gtt	cag	aaa	gaa	cgg	ata	ggg	gcc	ttt	cgt	cat	aaa	ttg	caa	gta	gca	2688
Val	Gln	Lys	Glu	Arg	Ile	Gly	Ala	Phe	Arg	His	Lys	Leu	Gln	Val	Ala	
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Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp  
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Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu  
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Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln  
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Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser  
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Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu  
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His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val  
110 115 120

Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser  
125 130 135

Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu  
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Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp  
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Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln  
175 180 185

Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe  
190 195 200

Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys  
205 210 215

Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser  
220 225 230 235

Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys  
240 245 250

Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val  
 255 260 265  
 Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe  
 270 275 280  
 Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly  
 285 290 295  
 Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln  
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 Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln  
 320 325 330  
 Trp Leu Lys Cys Ser Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro  
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 Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu  
 350 355 360  
 Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr  
 365 370 375  
 Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys  
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 Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His  
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 Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser  
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 Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro  
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 460 465 470 475  
 Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp  
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 495 500 505  
 Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg  
 510 515 520  
 Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly  
 525 530 535

Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu  
 540 545 550 555  
 Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp  
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 Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn  
 575 580 585  
 Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser  
 590 595 600  
 Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu  
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 Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp  
 620 625 630 635  
 Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser  
 640 645 650  
 Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val  
 655 660 665  
 Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu  
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 Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val  
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 Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val  
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 Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu  
 720 725 730  
 Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp  
 735 740 745  
 Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu  
 750 755 760  
 Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu  
 765 770 775  
 Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val  
 780 785 790 795  
 Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val  
 800 805 810  
 His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile  
 815 820 825



Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu  
830 835 840

Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro  
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Homo sapiens

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Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr  
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agc ttc ttc agt ttc cca gaa ctg cag gtg ctg gat tta tcc agg tgt 144  
Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys  
35 40 45

gaa atc cag aca att gaa gat ggg gca tat cag agc cta agc cac ctc 192  
Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu  
50 55 60

tct acc tta ata ttg aca gga aac ccc atc cag agt tta gcc ctg gga 240  
Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly  
65 70 75 80

gcc ttt tct gga cta tca agt tta cag aag ctg gtg gct gtg gag aca 288  
Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr  
85 90 95

aat cta gca tct cta gag aac ttc ccc att gga cat ctc aaa act ttg 336  
Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu

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115																				
gag Glu	tat Tyr	ttt Phe	tct Ser	aat Asn	ctg Leu	acc Thr	aat Asn	cta Leu	gag Glu	cac His	ttg Leu	gac Asp	ctt Leu	tcc Ser	agc Ser	432				
130																				
aac Asn	aag Lys	att Ile	caa Gln	agt Ser	att Ile	tat Tyr	tgc Cys	aca Thr	gac Asp	ttg Leu	cgg Arg	gtt Val	cta Leu	cat His	caa Gln	480				
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atg Met	ccc Pro	cta Leu	ctc Leu	aat Asn	ctc Leu	tct Ser	tta Leu	gac Asp	ctg Leu	tcc Ser	ctg Leu	aac Asn	cct Pro	atg Met	aac Asn	528				
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tta Leu	aga Arg	aat Asn	aat Asn	ttt Phe	gat Asp	agt Ser	tta Leu	aat Asn	gta Val	atg Met	aaa Lys	act Thr	tgt Cys	att Ile	caa Gln	624				
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245																				
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290																				
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305																				
310																				
315																				
320																				

aac	aaa	ggg	ggg	aat	gct	ttt	tca	gaa	gtt	gat	cta	cca	agc	ctt	gag	1008
Asn	Lys	Gly	Gly	Asn	Ala	Phe	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	
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Phe	Leu	Asp	Leu	Ser	Arg	Asn	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	
			340					345					350			
caa	agt	gat	ttt	ggg	aca	acc	agc	cta	aag	tat	tta	gat	ctg	agc	ttc	1104
Gln	Ser	Asp	Phe	Gly	Thr	Thr	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	
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aat	ggg	gtt	att	acc	atg	agt	tca	aac	ttc	ttg	ggc	tta	gaa	caa	cta	1152
Asn	Gly	Val	Ile	Thr	Met	Ser	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	
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Glu	His	Leu	Asp	Phe	Gln	His	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	
					390					395					400	
tca	gta	ttc	cta	tca	ctc	aga	aac	ctc	att	tac	ctt	gac	att	tct	cat	1248
Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	
					405				410					415		
acc	cac	acc	aga	ggt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	ttg	tcc	agt	1296
Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	
			420					425					430			
ctc	gaa	gtc	ttg	aaa	atg	gct	ggc	aat	tct	ttc	cag	gaa	aac	ttc	ctt	1344
Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	
			435				440					445				
caa	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	gac	ctc	tct	1392
Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	
			450			455					460					
cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	tca	ctc	tcc	1440
Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	
					470					475					480	
agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	tca	ttg	gat	1488
Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	
				485					490					495		
acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	gat	tac	agt	1536
Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	
			500					505					510			
ctc	aat	cac	ata	atg	act	tcc	aaa	aaa	cag	gaa	cta	cag	cat	ttt	cca	1584
Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	
			515				520					525				
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Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr		
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Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu		
545					550					555					560		
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Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln		
				565					570					575			
ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	aat	aag	acc	1776	
Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr		
			580					585					590				
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Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val	Ala		
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Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu		
				645					650					655			
gaa	gaa	ggg	gtg	cct	cca	ttt	cag	ctc	tgc	ctt	cac	tac	aga	gac	ttt	2016	
Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe		
			660					665					670				
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Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	Gly	Phe	His		
		675				680						685					
aaa	agc	cga	aag	gtg	att	gtt	gtg	gtg	tcc	cag	cac	ttc	atc	cag	agc	2112	
Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	Ile	Gln	Ser		
			690			695				700							
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Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu		
705					710				715					720			
agc	agt	cgt	gct	ggg	atc	atc	ttc	att	gtc	ctg	cag	aag	gtg	gag	aag	2208	
Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	Val	Glu	Lys		
			725					730					735				
acc	ctg	ctc	agg	cag	cag	gtg	gag	ctg	tac	cgc	ctt	ctc	agc	agg	aac	2256	
Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	Ser	Arg	Asn		

740										745					750					
act	tac	ctg	gag	tgg	gag	gac	agt	gtc	ctg	ggg	cgg	cac	atc	ttc	tgg	2304				
Thr	Tyr	Leu	Glu	Trp	Glu	Asp	Ser	Val	Leu	Gly	Arg	His	Ile	Phe	Trp					
		755					760					765								
aga	cga	ctc	aga	aaa	gcc	ctg	ctg	gat	ggg	aaa	tca	tgg	aat	cca	gaa	2352				
Arg	Arg	Leu	Arg	Lys	Ala	Leu	Leu	Asp	Gly	Lys	Ser	Trp	Asn	Pro	Glu					
		770				775					780									
gga	aca	gtg	ggg	aca	gga	tgc	aat	tgg	cag	gaa	gca	aca	tct	atc	tga	2400				
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Ser	Phe	Phe	Ser	Phe	Pro	Glu	Leu	Gln	Val	Leu	Asp	Leu	Ser	Arg	Cys
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Glu	Ile	Gln	Thr	Ile	Glu	Asp	Gly	Ala	Tyr	Gln	Ser	Leu	Ser	His	Leu
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Ser	Thr	Leu	Ile	Leu	Thr	Gly	Asn	Pro	Ile	Gln	Ser	Leu	Ala	Leu	Gly
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Ala	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Lys	Leu	Val	Ala	Val	Glu	Thr
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Asn	Leu	Ala	Ser	Leu	Glu	Asn	Phe	Pro	Ile	Gly	His	Leu	Lys	Thr	Leu
		100						105					110		
Lys	Glu	Leu	Asn	Val	Ala	His	Asn	Leu	Ile	Gln	Ser	Phe	Lys	Leu	Pro
		115					120					125			
Glu	Tyr	Phe	Ser	Asn	Leu	Thr	Asn	Leu	Glu	His	Leu	Asp	Leu	Ser	Ser
	130					135					140				
Asn	Lys	Ile	Gln	Ser	Ile	Tyr	Cys	Thr	Asp	Leu	Arg	Val	Leu	His	Gln
	145				150					155					160
Met	Pro	Leu	Leu	Asn	Leu	Ser	Leu	Asp	Leu	Ser	Leu	Asn	Pro	Met	Asn
				165					170					175	

Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr  
 180 185 190  
 Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln  
 195 200 205  
 Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg  
 210 215 220  
 Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu  
 225 230 235 240  
 Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr  
 245 250 255  
 Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser  
 260 265 270  
 Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr  
 275 280 285  
 Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln  
 290 295 300  
 Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser  
 305 310 315 320  
 Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu  
 325 330 335  
 Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser  
 340 345 350  
 Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe  
 355 360 365  
 Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu  
 370 375 380  
 Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe  
 385 390 395 400  
 Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His  
 405 410 415  
 Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser  
 420 425 430  
 Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu  
 435 440 445  
 Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser  
 450 455 460

Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	465	470	475	480
Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	485	490	495	
Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	500	505	510	
Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	515	520	525	
Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr	530	535	540	
Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu	545	550	555	560
Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln	565	570	575	
Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr	580	585	590	
Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val	Ala	595	600	605	
Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu	Ala	Gly	Cys	610	615	620	
Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	Asp	Ala	Phe	Val	Ile	Tyr	625	630	635	640
Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu	645	650	655	
Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe	660	665	670	
Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	Gly	Phe	His	675	680	685	
Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	Ile	Gln	Ser	690	695	700	
Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu	705	710	715	720
Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	Val	Glu	Lys	725	730	735	
Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	Ser	Arg	Asn	740	745	750	

Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp  
755 760 765

Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu  
770 775 780

Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile  
785 790 795

<210> 9

<211> 1275

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1) .. (1095)

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tgt tgg gat gtt ttt gag gga ctt tct cat ctt caa gtt ctg tat ttg 48  
Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu  
5 10 15

aat cat aac tat ctt aat tcc ctt cca cca gga gta ttt agc cat ctg 96  
Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu  
20 25 30

act gca tta agg gga cta agc ctc aac tcc aac agg ctg aca gtt ctt 144  
Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu  
35 40 45

tct cac aat gat tta cct gct aat tta gag atc ctg gac ata tcc agg 192  
Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg  
50 55 60

aac cag ctc cta gct cct aat cct gat gta ttt gta tca ctt agt gtc 240  
Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val  
65 70 75 80

ttg gat ata act cat aac aag ttc att tgt gaa tgt gaa ctt agc act 288  
Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr  
85 90 95

ttt atc aat tgg ctt aat cac acc aat gtc act ata gct ggg cct cct 336  
Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro  
100 105 110



gca gac ata tat tgt gtg tac cct gac tcg ttc tct ggg gtt tcc ctc Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu 115 120 125	384
ttc tct ctt tcc acg gaa ggt tgt gat gaa gag gaa gtc tta aag tcc Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser 130 135 140	432
cta aag ttc tcc ctt ttc att gta tgc act gtc act ctg act ctg ttc Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe 145 150 155 160	480
ctc atg acc atc ctc aca gtc aca aag ttc cgg ggc ttc tgt ttt atc Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile 165 170 175	528
tgt tat aag aca gcc cag aga ctg gtg ttc aag gac cat ccc cag ggc Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly 180 185 190	576
aca gaa cct gat atg tac aaa tat gat gcc tat ttg tgc ttc agc agc Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr Leu Cys Phe Ser Ser 195 200 205	624
aga gac ttc aca tgg gtg cag aat gct ttg ctc aaa cac ctg gac act Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr 210 215 220	672
caa tac agt gac caa aac aga ttc aac ctg tgc ttt gaa gaa aga gac Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp 225 230 235 240	720
ttt gtc cca gga gaa aac cgc att gcc aat atc cag gat gcc atc tgg Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp 245 250 255	768
aac agt aga aag atc gtt tgt ctt gtg agc aga cac ttc ctt aga gat Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp 260 265 270	816
ggc tgg tgc ctt gaa gcc ttc agt tat gcc cag ggc agg tgc tta tct Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser 275 280 285	864
gac ctt aac agt gct ctc atc atg gtg gtg gtt ggg tcc ttg tcc cag Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln 290 295 300	912
tac cag ttg atg aaa cat caa tcc atc aga ggc ttt gta cag aaa cag Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln 305 310 315 320	960
cag tat ttg agg tgg cct gag gat ctc cag gat gtt ggc tgg ttt ctt Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu	1008

325

330

335

cat aaa ctc tct caa cag ata cta aag aaa gaa aag gaa aag aag aaa 1056  
 His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys Lys  
                   340                  345                  350

gac aat aac att ccg ttg caa act gta gca acc atc tcc taatcaaagg 1105  
 Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser  
                   355                  360                  365

agcaatttcc aacttatctc aagccacaaa taactcttca ctttgtattt gcaccaagtt 1165

atcattttgg ggtcctctct ggaggttttt tttttctttt tgctactatg aaaacaacat 1225

aaatctctca attttcgtat caaaaaaaaa aaaaaaaaaa tggcggccgc 1275

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<211> 365

<212> PRT

<213> Unknown

<400> 10

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Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu  
                   20                  25                  30

Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu  
                   35                  40                  45

Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg  
                   50                  55                  60

Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val  
                   65                  70                  75                  80

Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr  
                   85                  90                  95

Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro  
                   100                  105                  110

Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu  
                   115                  120                  125

Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser  
                   130                  135                  140

Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe  
                   145                  150                  155                  160

Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile  
 165 170 175  
 Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly  
 180 185 190  
 Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr Leu Cys Phe Ser Ser  
 195 200 205  
 Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr  
 210 215 220  
 Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp  
 225 230 235 240  
 Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp  
 245 250 255  
 Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp  
 260 265 270  
 Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser  
 275 280 285  
 Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln  
 290 295 300  
 Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln  
 305 310 315 320  
 Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu  
 325 330 335  
 His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys  
 340 345 350  
 Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser  
 355 360 365

<210> 11

<211> 3138

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(3135)

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Met	Trp	Thr	Leu	Lys	Arg	Leu	Ile	Leu	Ile	Leu	Phe	Asn	Ile	Ile	Leu	
		-20					-15					-10				

att	tcc	aaa	ctc	ctt	ggg	gct	aga	tgg	ttt	cct	aaa	act	ctg	ccc	tgt	96
Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	Pro	Lys	Thr	Leu	Pro	Cys	
	-5				-1	1				5					10	

gat	gtc	act	ctg	gat	gtt	cca	aag	aac	cat	gtg	atc	gtg	gac	tgc	aca	144
Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	His	Val	Ile	Val	Asp	Cys	Thr	
			15						20					25		

gac	aag	cat	tgt	aca	gaa	att	cct	gga	ggt	att	ccc	acg	aac	acc	acg	192
Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	
			30					35					40			

aac	ctc	acc	ctc	acc	att	aac	cac	ata	cca	gac	atc	tcc	cca	gcg	tcc	240
Asn	Leu	Thr	Leu	Thr	Ile	Asn	His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	
		45					50					55				

ttt	cac	aga	ctg	gac	cat	ctg	gta	gag	atc	gat	ttc	aga	tgc	aac	tgt	288
Phe	His	Arg	Leu	Asp	His	Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	
	60				65					70						

gta	cct	att	cca	ctg	ggg	tca	aaa	aac	aac	atg	tgc	atc	aag	agg	ctg	336
Val	Pro	Ile	Pro	Leu	Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	
	75				80					85					90	

cag	att	aaa	ccc	aga	agc	ttt	agt	gga	ctc	act	tat	tta	aaa	tcc	ctt	384
Gln	Ile	Lys	Pro	Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	
			95					100						105		

tac	ctg	gat	gga	aac	cag	cta	cta	gag	ata	cgg	cag	ggc	ctc	cgg	cct	432
Tyr	Leu	Asp	Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	
			110					115					120			

agc	tta	cag	ctt	ctc	agc	ctt	gag	gcc	aac	aac	atc	ttt	tcc	atc	aga	480
Ser	Leu	Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	
		125					130					135				

aaa	gag	aat	cta	aca	gaa	ctg	gcc	aac	ata	gaa	ata	ctc	tac	ctg	ggc	528
Lys	Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	
	140					145					150					

caa	aac	tgt	tat	tat	cga	aat	cct	tgt	tat	gtt	tca	tat	tca	ata	gag	576
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	Glu	
	155				160					165					170	

aaa	gat	gcc	ttc	cta	aac	ttg	aca	aag	tta	aaa	gtg	ctc	tcc	ctg	aaa	624
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Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser	Leu	Lys		
				175					180					185			
gat	aac	aat	gtc	aca	gcc	gtc	cct	act	ggt	ttg	cca	tct	act	tta	aca	672	
Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	Thr	Leu	Thr		
			190					195					200				
gaa	cta	tat	ctc	tac	aac	aac	atg	att	gca	aaa	atc	caa	gaa	gat	gat	720	
Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	Gln	Glu	Asp	Asp		
		205					210					215					
ttt	aat	aac	ctc	aac	caa	tta	caa	att	ctt	gac	cta	agt	gga	aat	tcg	768	
Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp	Leu	Ser	Gly	Asn	Cys		
		220				225					230						
cct	cg	tgt	tat	aat	gcc	cca	ttt	cct	tgt	gcg	ccg	tgt	aaa	aat	aat	816	
Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	Ala	Pro	Cys	Lys	Asn	Asn		
235					240					245				250			
tct	ccc	cta	cag	atc	cct	gta	aat	gct	ttt	gat	gcg	ctg	aca	gaa	tta	864	
Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	Leu	Thr	Glu	Leu		
				255					260					265			
aaa	ggt	tta	cg	cta	cac	agt	aac	tct	ctt	cag	cat	gtg	ccc	cca	aga	912	
Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	Val	Pro	Pro	Arg		
			270					275					280				
tgg	ttt	aag	aac	atc	aac	aaa	ctc	cag	gaa	ctg	gat	ctg	tcc	caa	aac	960	
Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn		
		285					290					295					
ttc	ttg	gcc	aaa	gaa	att	ggg	gat	gct	aaa	ttt	ctg	cat	ttt	ctc	ccc	1008	
Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro		
		300				305					310						
agc	ctc	atc	caa	ttg	gat	ctg	tct	ttc	aat	ttt	gaa	ctt	cag	gtc	tat	1056	
Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr		
315					320					325				330			
cg	gca	tct	atg	aat	cta	tca	caa	gca	ttt	tct	tca	ctg	aaa	agc	ctg	1104	
Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu		
				335				340					345				
aaa	att	ctg	cg	atc	aga	gga	tat	gtc	ttt	aaa	gag	ttg	aaa	agc	ttt	1152	
Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe		
			350					355					360				
aac	ctc	tcg	cca	tta	cat	aat	ctt	caa	aat	ctt	gaa	ggt	ctt	gat	ctt	1200	
Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu		
			365				370					375					
ggc	act	aac	ttt	ata	aaa	att	gct	aac	ctc	agc	atg	ttt	aaa	caa	ttt	1248	
Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe		
		380				385					390						

aaa Lys 395	aga Arg	ctg Leu	aaa Lys	gtc Val	ata Ile	gat Asp	ctt Leu	tca Ser	gtg Val	aat Asn	aaa Lys	ata Ile	tca Ser	cct Pro	tca Ser	1296
gga Gly	gat Asp	tca Ser	agt Ser	gaa Glu	gtt Val	ggc Gly	ttc Phe	tgc Cys	tca Ser	aat Asn	gcc Ala	aga Arg	act Thr	tct Ser	gta Val	1344
gaa Glu	agt Ser	tat Tyr	gaa Glu	ccc Pro	cag Gln	gtc Val	ctg Leu	gaa Glu	caa Gln	tta Leu	cat His	tat Tyr	ttc Phe	aga Arg	tat Tyr	1392
gat Asp	aag Lys	tat Tyr	gca Ala	agg Arg	agt Ser	tgc Cys	aga Arg	ttc Phe	aaa Lys	aac Asn	aaa Lys	gag Glu	gct Ala	tct Ser	ttc Phe	1440
atg Met	tct Ser	gtt Val	aat Asn	gaa Glu	agc Ser	tgc Cys	tac Tyr	aag Lys	tat Tyr	ggg Gly	cag Gln	acc Thr	ttg Leu	gat Asp	cta Leu	1488
agt Ser	aaa Lys	aat Asn	agt Ser	ata Ile	ttt Phe	ttt Phe	gtc Val	aag Lys	tcc Ser	tct Ser	gat Asp	ttt Phe	cag Gln	cat His	ctt Leu	1536
tct Ser	ttc Phe	ctc Leu	aaa Lys	tgc Cys	ctg Leu	aat Asn	ctg Leu	tca Ser	gga Gly	aat Asn	ctc Leu	att Ile	agc Ser	caa Gln	act Thr	1584
ctt Leu	aat Asn	ggc Gly	agt Ser	gaa Glu	ttc Phe	caa Gln	cct Pro	tta Leu	gca Ala	gag Glu	ctg Leu	aga Arg	tat Tyr	ttg Leu	gac Asp	1632
ttc Phe	tcc Ser	aac Asn	aac Asn	cgg Arg	ctt Leu	gat Asp	tta Leu	ctc Leu	cat His	tca Ser	aca Thr	gca Ala	ttt Phe	gaa Glu	gag Glu	1680
ctt Leu	cac His	aaa Lys	ctg Leu	gaa Glu	gtt Val	ctg Leu	gat Asp	ata Ile	agc Ser	agt Ser	aat Ser	agc Ser	cat His	tat Tyr	ttt Phe	1728
caa Gln	tca Ser	gaa Glu	gga Gly	att Ile	act Thr	cat His	atg Met	cta Leu	aac Asn	ttt Phe	acc Thr	aag Lys	aac Asn	cta Leu	aag Lys	1776
gtt Val	ctg Leu	cag Gln	aaa Lys	ctg Leu	atg Met	atg Met	aac Asn	gac Asp	aat Asn	gac Asp	atc Ile	tct Ser	tcc Ser	tcc Ser	acc Thr	1824
agc Ser	agg Arg	acc Thr	atg Met	gag Glu	agt Ser	gag Glu	tct Ser	ctt Leu	aga Arg	act Thr	ctg Leu	gaa Glu	ttc Phe	aga Arg	gga Gly	1872

aat Asn	cac His	tta Leu 605	gat Asp	gtt Val	tta Leu	tgg Trp	aga Arg 610	gaa Glu	ggt Gly	gat Asp	aac Asn	aga Arg 615	tac Tyr	tta Leu	caa Gln	1920
tta Leu	ttc Phe 620	aag Lys	aat Asn	ctg Leu	cta Leu	aaa Lys 625	tta Leu	gag Glu	gaa Glu	tta Leu	gac Asp 630	atc Ile	tct Ser	aaa Lys	aat Asn	1968
tcc Ser 635	cta Leu	agt Ser	ttc Phe	ttg Leu	cct Pro 640	tct Ser	gga Gly	gtt Val	ttt Phe	gat Asp 645	ggt Gly	atg Met	cct Pro	cca Pro	aat Asn 650	2016
cta Leu	aag Lys	aat Asn	ctc Leu	tct Ser 655	ttg Leu	gcc Ala	aaa Lys	aat Asn	ggg Gly 660	ctc Leu	aaa Lys	tct Ser	ttc Phe	agt Ser 665	tgg Trp	2064
aag Lys	aaa Lys	ctc Leu	cag Gln 670	tgt Cys	cta Leu	aag Lys	aac Asn	ctg Leu 675	gaa Glu	act Thr	ttg Leu	gac Asp	ctc Leu 680	agc Ser	cac His	2112
aac Asn	caa Gln	ctg Leu	acc Thr	act Thr	gtc Val	cct Pro	gag Glu 690	aga Arg	tta Leu	tcc Ser	aac Asn	tgt Cys 695	tcc Ser	aga Arg	agc Ser	2160
ctc Leu	aag Lys 700	aat Asn	ctg Leu	att Ile	ctt Leu	aag Lys 705	aat Asn	aat Asn	caa Gln	atc Ile	agg Arg 710	agt Ser	ctg Leu	acg Thr	aag Lys	2208
tat Tyr 715	ttt Phe	cta Leu	caa Gln	gat Asp	gcc Ala 720	ttc Phe	cag Gln	ttg Leu	cga Arg	tat Tyr 725	ctg Leu	gat Asp	ctc Leu	agc Ser	tca Ser 730	2256
aat Asn	aaa Lys	atc Ile	cag Gln	atg Met 735	atc Pro	caa Gln	aag Lys	acc Thr	agc Ser 740	ttc Phe	cca Pro	gaa Glu	aat Asn	gtc Val 745	ctc Leu	2304
aac Asn	aat Asn	ctg Leu	aag Lys 750	atg Met	ttg Leu	ctt Leu	ttg Leu	cat His 755	cat His	aat Asn	cgg Arg	ttt Phe	ctg Leu 760	tgc Cys	acc Thr	2352
tgt Cys	gat Asp	gct Ala 765	gtg Val	tgg Trp	ttt Phe	gtc Val	tgg Trp 770	tgg Trp	gtt Val	aac Asn	cat His	acg Thr 775	gag Glu	gtg Val	act Thr	2400
att Ile	cct Pro 780	tac Tyr	ctg Leu	gcc Ala	aca Thr	gat Asp 785	gtg Val	act Thr	tgt Cys	gtg Val	ggg Gly 790	cca Pro	gga Gly	gca Ala	cac His	2448
aag Lys 795	ggc Gly	caa Gln	agt Ser	gtg Val	atc Ile 800	tcc Ser	ctg Leu	gat Asp	ctg Leu	tac Tyr 805	acc Thr	tgt Cys	gag Glu	tta Leu	gat Asp 810	2496
ctg Leu	act Asn	aac Asn	ctg Leu	att Ile	ctg Leu	ttc Phe	tca Ser	ctt Leu	tcc Ser	ata Ile	tct Ser	gta Val	tct Ser	ctc Leu	ttt Phe	2544

815										820										825																				
ctc	atg	gtg	atg	atg	aca	gca	agt	cac	ctc	tat	ttc	tgg	gat	gtg	tgg	2592																								
Leu	Met	Val	Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp																									
830										835										840																				
tat	att	tac	cat	ttc	tgt	aag	gcc	aag	ata	aag	ggg	tat	cag	cgt	cta	2640																								
Tyr	Ile	Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu																									
845										850										855																				
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Ile	Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys																									
860										865										870																				
gac	cca	gct	gtg	acc	gag	tgg	ggt	ttg	gct	gag	ctg	gtg	gcc	aaa	ctg	2736																								
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	Leu																									
875										880										885										890										
gaa	gac	cca	aga	gag	aaa	cat	ttt	aat	tta	tgt	ctc	gag	gaa	agg	gac	2784																								
Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	Arg	Asp																									
895										900										905																				
tgg	tta	cca	ggg	cag	cca	ggt	ctg	gaa	aac	ctt	tcc	cag	agc	ata	cag	2832																								
Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	Ser	Ile	Gln																									
910										915										920																				
ctt	agc	aaa	aag	aca	gtg	ttt	gtg	atg	aca	gac	aag	tat	gca	aag	act	2880																								
Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	Tyr	Ala	Lys	Thr																									
925										930										935																				
gaa	aat	ttt	aag	ata	gca	ttt	tac	ttg	tcc	cat	cag	agg	ctc	atg	gat	2928																								
Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	Gln	Arg	Leu	Met	Asp																									
940										945										950																				
gaa	aaa	ggt	gat	gtg	att	atc	ttg	ata	ttt	ctt	gag	aag	ccc	ttt	cag	2976																								
Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	Leu	Glu	Lys	Pro	Phe	Gln																									
955										960										965										970										
aag	tcc	aag	ttc	ctc	cag	ctc	cgg	aaa	agg	ctc	tgt	ggg	agt	tct	gtc	3024																								
Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	Leu	Cys	Gly	Ser	Ser	Val																									
975										980										985																				
ctt	gag	tgg	cca	aca	aac	ccg	caa	gct	cac	cca	tac	ttc	tgg	cag	tgt	3072																								
Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys																									
990										995										1000																				
cta	aag	aac	gcc	ctg	gcc	aca	gac	aat	cat	gtg	gcc	tat	agt	cag	gtg	3120																								
Leu	Lys	Asn	Ala	Leu	Ala	Thr	Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val																									
1005										1010										1015																				
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Phe	Lys	Glu	Thr	Val																																				
1020																																								



<210> 12  
<211> 1045  
<212> PRT  
<213> Unknown

<400> 12

Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu  
-20 -15 -10

Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys  
-5 -1 1 5 10

Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr  
15 20 25

Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr  
30 35 40

Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser  
45 50 55

Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys  
60 65 70

Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu  
75 80 85 90

Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu  
95 100 105

Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro  
110 115 120

Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg  
125 130 135

Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
140 145 150

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu  
155 160 165 170

Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser Leu Lys  
175 180 185

Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser Thr Leu Thr  
190 195 200

Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile Gln Glu Asp Asp  
205 210 215

Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu Ser Gly Asn Cys

220		225		230
Pro Arg Cys Tyr Asn Ala	Pro Phe Pro Cys Ala	Pro Cys Lys Asn Asn		
235	240	245	250	
Ser Pro Leu Gln Ile	Pro Val Asn Ala Phe Asp Ala	Leu Thr Glu Leu		
255	260	265		
Lys Val Leu Arg Leu His Ser Asn Ser	Leu Gln His Val	Pro Pro Arg		
270	275	280		
Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp	Leu Ser Gln Asn			
285	290	295		
Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu His Phe Leu Pro				
300	305	310		
Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr				
315	320	325		330
Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu				
335	340	345		
Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe				
350	355	360		
Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu				
365	370	375		
Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe				
380	385	390		
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro Ser				
395	400	405		410
Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr Ser Val				
415	420	425		
Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr Phe Arg Tyr				
430	435	440		
Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys Glu Ala Ser Phe				
445	450	455		
Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln Thr Leu Asp Leu				
460	465	470		
Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp Phe Gln His Leu				
475	480	485		490
Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu Ile Ser Gln Thr				
495	500	505		

Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu Arg Tyr Leu Asp  
 510 515 520  
 Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu  
 525 530 535  
 Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe  
 540 545 550  
 Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys  
 555 560 565 570  
 Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr  
 575 580 585  
 Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly  
 590 595 600  
 Asn His Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln  
 605 610 615  
 Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn  
 620 625 630  
 Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro Asn  
 635 640 645 650  
 Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe Ser Trp  
 655 660 665  
 Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp Leu Ser His  
 670 675 680  
 Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn Cys Ser Arg Ser  
 685 690 695  
 Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg Ser Leu Thr Lys  
 700 705 710  
 Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu Asp Leu Ser Ser  
 715 720 725 730  
 Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro Glu Asn Val Leu  
 735 740 745  
 Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg Phe Leu Cys Thr  
 750 755 760  
 Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His Thr Glu Val Thr  
 765 770 775  
 Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly Pro Gly Ala His  
 780 785 790

Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp  
 795 800 805 810  
 Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe  
 815 820 825  
 Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp  
 830 835 840  
 Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu  
 845 850 855  
 Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
 860 865 870  
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys Leu  
 875 880 885 890  
 Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu Arg Asp  
 895 900 905  
 Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln Ser Ile Gln  
 910 915 920  
 Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr  
 925 930 935  
 Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp  
 940 945 950  
 Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln  
 955 960 965 970  
 Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val  
 975 980 985  
 Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys  
 990 995 1000  
 Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val  
 1005 1010 1015  
 Phe Lys Glu Thr Val  
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<210> 13

<211> 180

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: rodent; surmised

Mus musculus

<220>

<221> CDS

<222> (1)..(177)

<400> 13

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Leu Gly Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg  
1 5 10 15

ctc tgc agg agc tct gtc ctt gag tgg cct gca aat cca cag gct cac 96  
Leu Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His  
20 25 30

cca tac ttc tgg cag tgc ctg aaa aat gcc ctg acc aca gac aat cat 144  
Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His  
35 40 45

gtg gct tat agt caa atg ttc aag gaa aca gtc tag 180  
Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val  
50 55

<210> 14

<211> 59

<212> PRT

<213> Unknown

<400> 14

Leu Gly Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg  
1 5 10 15

Leu Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His  
20 25 30

Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His  
35 40 45

Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val  
50 55

<210> 15

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (2) .. (988)

<400> 15

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Asn	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn	Cys		
1				5					10					15			
tat	ttt	aac	aaa	gtt	tgc	gag	aaa	act	aac	ata	gaa	gat	gga	gta	ttt	97	
Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly	Val	Phe		
		20					25					30					
gaa	acg	ctg	aca	aat	ttg	gag	ttg	cta	tca	cta	tct	ttc	aat	tct	ctt	145	
Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe	Asn	Ser	Leu		
		35				40						45					
tca	cat	gtg	cca	ccc	aaa	ctg	cca	agc	tcc	cta	cgc	aaa	ctt	ttt	ctg	193	
Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg	Lys	Leu	Phe	Leu		
	50				55					60							
agc	aac	acc	cag	atc	aaa	tac	att	agt	gaa	gaa	gat	ttc	aag	gga	ttg	241	
Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu	Asp	Phe	Lys	Gly	Leu		
	65				70				75					80			
ata	aat	tta	aca	tta	cta	gat	tta	agc	ggg	aac	tgt	ccg	agg	tgc	ttc	289	
Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Phe		
				85					90					95			
aat	gcc	cca	ttt	cca	tgc	gtg	cct	tgt	gat	ggg	ggg	gct	tca	att	aat	337	
Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys	Asp	Gly	Gly	Ala	Ser	Ile	Asn		
			100				105						110				
ata	gat	cgt	ttt	gct	ttt	caa	aac	ttg	acc	caa	ctt	cga	tac	cta	aac	385	
Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn	Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn		
		115				120						125					
ctc	tct	agc	act	tcc	ctc	agg	aag	att	aat	gct	gcc	tgg	ttt	aaa	aat	433	
Leu	Ser	Ser	Thr	Ser	Leu	Arg	Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn		
		130				135					140						
atg	cct	cat	ctg	aag	gtg	ctg	gat	ctt	gaa	ttc	aac	tat	tta	gtg	gga	481	
Met	Pro	His	Leu	Lys	Val	Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly		
	145				150				155					160			
gaa	ata	gcc	tct	ggg	gca	ttt	tta	acg	atg	ctg	ccc	cgc	tta	gaa	ata	529	
Glu	Ile	Ala	Ser	Gly	Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile		
				165					170					175			
ctt	gac	ttg	tct	ttt	aac	tat	ata	aag	ggg	agt	tat	cca	cag	cat	att	577	
Leu	Asp	Leu	Ser	Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile		
			180					185					190				
aat	att	tcc	aga	aac	ttc	tct	aaa	ctt	ttg	tct	cta	cgg	gca	ttg	cat	625	
Asn	Ile	Ser	Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His		

195	200	205	
tta aga ggt tat gtg ttc cag gaa ctc aga gaa gat gat ttc cag ccc	673		
Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Phe Gln Pro			
210	215	220	
ctg atg cag ctt cca aac tta tcg act atc aac ttg ggt att aat ttt	721		
Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe			
225	230	235	240
att aag caa atc gat ttc aaa ctt ttc caa aat ttc tcc aat ctg gaa	769		
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu			
245	250	255	
att att tac ttg tca gaa aac aga ata tca ccg ttg gta aaa gat acc	817		
Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr			
260	265	270	
cgg cag agt tat gca aat agt tcc tct ttt caa cgt cat atc cgg aaa	865		
Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys			
275	280	285	
cga cgc tca aca gat ttt gag ttt gac cca cat tcg aac ttt tat cat	913		
Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His			
290	295	300	
tcc acc cgt cct tta ata aag cca caa tgt gct gct tat gga aaa gcc	961		
Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala			
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tta gat tta agc ctc aac agt att ttc tt	990		
Leu Asp Leu Ser Leu Asn Ser Ile Phe			
325			
<210> 16			
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<400> 16			
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Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe			
20	25	30	
Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu			
35	40	45	
Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu			
50	55	60	
Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu			

65	70	75	80
Ile Asn Leu Thr	Leu Leu Asp Leu Ser	Gly Asn Cys Pro Arg Cys Phe	
	85	90	95
Asn Ala Pro Phe	Pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn		
100	105	110	
Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn			
115	120	125	
Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn			
130	135	140	
Met Pro His Leu Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly			
145	150	155	160
Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile			
	165	170	175
Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile			
	180	185	190
Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His			
	195	200	205
Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro			
	210	215	220
Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe			
225	230	235	240
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu			
	245	250	255
Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr			
	260	265	270
Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys			
	275	280	285
Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His			
	290	295	300
Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala			
305	310	315	320
Leu Asp Leu Ser Leu Asn Ser Ile Phe			
	325		

<210> 17

<211> 1557



<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(513)

<220>

<221> misc feature

<222> (93)..(149)

<223> Xaa translation depends on genetic code

<400> 17

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Gln	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser	Tyr	
1				5					10					15		

gac	acc	aaa	gat	gcc	tct	ggt	act	gac	tgg	gtg	ata	aat	gag	ctg	cgc	96
Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	Leu	Arg	
			20					25					30			

tac	cac	ctt	gaa	gag	agc	cga	gac	aaa	aac	ggt	ctc	ctt	tgt	cta	gag	144
Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu	Cys	Leu	Glu	
		35					40					45				

gag	agg	gat	tgg	gac	ccg	gga	ttg	gcc	atc	atc	gac	aac	ctc	atg	cag	192
Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp	Asn	Leu	Met	Gln	
	50					55					60					

agc	atc	aac	caa	agc	aag	aaa	aca	gta	ttt	ggt	tta	acc	aaa	aaa	tat	240
Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	Leu	Thr	Lys	Lys	Tyr	
65					70					75				80		

gca	aaa	agc	tgg	aac	ttt	aaa	aca	gct	ttt	tac	ttg	gsc	ttg	cag	agg	288
Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe	Tyr	Leu	Xaa	Leu	Gln	Arg	
				85					90					95		

cta	atg	ggt	gag	aac	atg	gat	gtg	att	ata	ttt	atc	ctg	ctg	gag	cca	336
Leu	Met	Gly	Glu	Asn	Met	Asp	Val	Ile	Ile	Phe	Ile	Leu	Leu	Glu	Pro	
		100						105					110			

gtg	tta	cag	cat	tct	ccg	tat	ttg	agg	cta	cgg	cag	cgg	atc	tgt	aag	384
Val	Leu	Gln	His	Ser	Pro	Tyr	Leu	Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	
		115				120						125				

agc	tcc	atc	ctc	cag	tgg	cct	gac	aac	ccg	aag	gca	gaa	agg	ttg	ttt	432
Ser	Ser	Ile	Leu	Gln	Trp	Pro	Asp	Asn	Pro	Lys	Ala	Glu	Arg	Leu	Phe	
		130				135					140					

tgg	caa	act	ctg	wga	aat	gtg	gtc	ttg	act	gaa	aat	gat	tca	cgg	tat	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Trp	Gln	Thr	Leu	Xaa	Asn	Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	
145					150					155					160	

aac aat atg tat gtc gat tcc att aag caa tac taactgacgt taagtcatga 533  
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr  
 165 170

tttcgcgcga taataaagat gcaaaggaat gacatttcng tattagttat ctattgctan 593  
 ggtaacnaaa ttantcccaa aaancttang tnggtttnaa aacaacnaca ttntgctggn 653  
 cccacagttt ttgaggggtca ggagtcagg cccagcataa ctgggtcttc tgcttcaggg 713  
 tgtctncaga ggctgcaatg taggtgttca ccagagacat aggcatcact ggggtcacac 773  
 tncatgtggg tgttttctgg attcaattcc tctgggcta ttggccaaag gctatactca 833  
 tgtaagccat gcgagcctat ccacaaangg cagcttgctt catcagagct agcaaaaaag 893  
 agaggttget agcaagatga agtcacaatc ttttgtaatc gaatcaaaaa agtgatatct 953  
 catcactttg gccatattct atttggttaga agtaaaccac aggtcccacc agctccatgg 1013  
 ggtgaccac ctacgtccag ggaaacacg tgaagaccaa gatgggtgagc tctgattgct 1073  
 tcatgttgct atcaactatt ttcccttgac tgctgtcctg ggatggccgg ctatcttgat 1133  
 ggtagattg tgaatatcag gaggccagg atcactgtgg accatcttag cagttgacct 1193  
 aacacatctt cttttcaata tctaagaact ttggccactg tgactaatgg tcctaataatt 1253  
 aagctgttgt ttatatattat catatatcta tggctacatg gttatattat gctgtggttg 1313  
 ggttcggtt tatttacagt tgcttttaca aatatttgct gtaacatttg acttctaagg 1373  
 tttagatgcc atttaagaac tgagatggat agctttttaa gcatctttta cttcttacca 1433  
 ttttttaaaa gtatgcagct aaattcgaag cttttggtct atattgttaa ttgccattgc 1493  
 tgtaaatctt aaaaatgaatg aataaaaatg tttcatttta aaaaaaaaaa aaaaaaaaaa 1553  
 aaaa 1557

<210> 18  
 <211> 171  
 <212> PRT  
 <213> Unknown

<400> 18															
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1					5				10					15	

Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg  
                   20                  25                  30  
 Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu  
                   35                  40                  45  
 Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln  
                   50                  55                  60  
 Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr  
                   65                  70                  75                  80  
 Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg  
                   85                  90                  95  
 Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro  
                   100                  105                  110  
 Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys  
                   115                  120                  125  
 Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe  
                   130                  135                  140  
 Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr  
                   145                  150                  155                  160  
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr  
                   165                  170

<210> 19  
 <211> 629  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(486)

<220>  
 <221> misc\_feature  
 <222> (48)..(75)  
 <223> Xaa translation depends on genetic code

<400> 19  
 aat gaa ttg atc ccc aat cta gag aag gaa gat ggt tct atc ttg att  
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile  
   1                  5                  10                  15

48

tgc ctt tat gaa agc tac ttt gac cct ggc aaa agc att agt gaa aat	96
Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn	
20 25 30	
att gta agc ttc att gag aaa agc tat aag tcc atc ttt gtt ttg tcy	144
Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa	
35 40 45	
ccc aac ttt gtc cag aat gag tgg tgc cat tat gaa ttc tac ttt gcc	192
Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala	
50 55 60	
cac cac aat ctc ttc cat gaa aat tct gat cay ata att ctt atc tta	240
His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu	
65 70 75 80	
ctg gaa ccc att cca ttc tat tgc att ccc acc agg tat cat aaa ctg	288
Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu	
85 90 95	
gaa gct ctc ctg gaa aaa aaa gca tac ttg gaa tgg ccc aag gat agg	336
Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg	
100 105 110	
aaa tgt ggg ctt ttc tgg gca aac ctt cga gct gct gtt aat gtt	384
Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Val Asn Val	
115 120 125	
aat gta tta gcc acc aga gaa atg tat gaa ctg cag aca ttc aca gag	432
Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu	
130 135 140	
tta aat gaa gag tct cga ggt tct aca atc tct ctg atg aga aca gac	480
Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp	
145 150 155 160	
tgt cta taaaatccca cagtccttgg gaagttgggg accacataca ctgttgggat	536
Cys Leu	
gtacattgat acaaccttta tgatggcaat ttgacaatat ttattaaaaat aaaaaatggg	596
tattcccttc aaaaaaaaaa aaaaaaaaaa aaa	629

<210> 20  
 <211> 162  
 <212> PRT  
 <213> Unknown

<400> 20  
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile  
 1 5 10 15

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Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn
      20                      25                      30
Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa
      35                      40                      45
Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala
      50                      55                      60
His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu
      65                      70                      75                      80
Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu
      85                      90                      95
Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg
      100                      105                      110
Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val
      115                      120                      125
Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu
      130                      135                      140
Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp
      145                      150                      155                      160
Cys Leu

<210> 21
<211> 427
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
      Homo sapiens

<220>
<221> CDS
<222> (1)..(426)

<400> 21
aag aac tcc aaa gaa aac ctc cag ttt cat gct ttt att tca tat agt      48
Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser
      1                      5                      10                      15
gaa cat gat tct gcc tgg gtg aaa agt gaa ttg gta cct tac cta gaa      96
Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu
      20                      25                      30
aaa gaa gat ata cag att tgt ctt cat gag aga aac ttt gtc cct ggc      144

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Lys	Glu	Asp	Ile	Gln	Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly		
		35					40					45					
aag	agc	att	gtg	gaa	aat	atc	atc	aac	tgc	att	gag	aag	agt	tac	aag	192	
Lys	Ser	Ile	Val	Glu	Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys		
	50				55					60							
tcc	atc	ttt	gtt	ttg	tct	ccc	aac	ttt	gtc	cag	agt	gag	tgg	tgc	cat	240	
Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His		
65				70					75					80			
tac	gaa	ctc	tat	ttt	gcc	cat	cac	aat	ctc	ttt	cat	gaa	gga	tct	aat	288	
Tyr	Glu	Leu	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn		
			85						90					95			
aac	tta	atc	ctc	atc	tta	ctg	gaa	ccc	att	cca	cag	aac	agc	att	ccc	336	
Asn	Leu	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro		
			100					105					110				
aac	aag	tac	cac	aag	ctg	aag	gct	ctc	atg	acg	cag	cgg	act	tat	ttg	384	
Asn	Lys	Tyr	His	Lys	Leu	Lys	Ala	Leu	Met	Thr	Gln	Arg	Thr	Tyr	Leu		
		115					120					125					
dag	tgg	ccc	aag	gag	aaa	agc	aaa	cg	ggg	ctc	ttt	tgg	gct	a		427	
Gln	Trp	Pro	Lys	Glu	Lys	Ser	Lys	Arg	Gly	Leu	Phe	Trp	Ala				
	130				135					140							

<210> 22  
 <211> 142  
 <212> PRT  
 <213> Unknown

Lys	Asn	Ser	Lys	Glu	Asn	Leu	Gln	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser		
1				5				10						15			
Glu	His	Asp	Ser	Ala	Trp	Val	Lys	Ser	Glu	Leu	Val	Pro	Tyr	Leu	Glu		
		20					25						30				
Lys	Glu	Asp	Ile	Gln	Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly		
		35					40					45					
Lys	Ser	Ile	Val	Glu	Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys		
	50				55					60							
Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His		
65				70					75					80			
Tyr	Glu	Leu	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn		
			85					90						95			
Asn	Leu	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro		

100

105

110

Asn Lys Tyr His Lys Leu Lys Ala Leu Met Thr Gln Arg Thr Tyr Leu  
 115 120 125

Gln Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe Trp Ala  
 130 135 140

&lt;210&gt; 23

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(627)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (18)..(136)

&lt;223&gt; Xaa translation depends on genetic code

&lt;400&gt; 23

gct tcc acc tgt gcc tgg cct ggc ttc cct ggc ggg ggc ggc aaa gtg 48  
 Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Gly Lys Val  
 5 10 15

ggc gar atg agg atg ccc tgc cct acg atg cct tcg tgg tct tcg aca 96  
 Gly Xaa Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Ser Thr  
 20 25 30

aaa cgc rga cgc cag tgg cag act ggg tgt aca acg agc ttc ggg ggc 144  
 Lys Arg Xaa Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly  
 35 40 45

agc tgg agg agt gcc gtg ggc gct ggg cac tcc gcc tgt gcc tgg agg 192  
 Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg  
 50 55 60

aac cgc act ggc tgc ctg gca aaa ccc tct ttg aga acc tgt ggg cct 240  
 Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro  
 65 70 75 80

cgg tct atg gca gcc gca aga cgc tgt ttg tgc tgg ccc aca cgg acc 288  
 Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr  
 85 90 95

ggg tca gtg gtc tct tgc gcg cca ktt ntc ctg ctg gcc cag cag cgc 336  
 Gly Ser Val Val Ser Cys Ala Pro Xaa Xaa Leu Leu Ala Gln Gln Arg

100										105										110																			
ctg	ctg	gar	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	atc	cta	ang	cct	384																							
Leu	Leu	Xaa	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	Ile	Leu	Xaa	Pro																								
115										120										125																			
gac	ggc	caa	gcc	tcc	cga	cta	cmn	gat	gcg	ctg	acc	agc	gcc	tct	gcc	432																							
Asp	Gly	Gln	Ala	Ser	Arg	Leu	Xaa	Asp	Ala	Leu	Thr	Ser	Ala	Ser	Ala																								
130										135										140																			
gcc	aga	gtg	tcc	tcc	tct	ggc	ccc	acc	agc	cca	gtg	gtc	gcg	cag	ctt	480																							
Ala	Arg	Val	Ser	Ser	Ser	Gly	Pro	Thr	Ser	Pro	Val	Val	Ala	Gln	Leu																								
145										150										155																			
ctg	agg	cca	gca	tgc	atg	gcc	ctg	acc	agg	gac	aac	cac	cac	ttc	tat	528																							
Leu	Arg	Pro	Ala	Cys	Met	Ala	Leu	Thr	Arg	Asp	Asn	His	His	Phe	Tyr																								
165										170										175																			
aac	cgg	aac	ttc	tgc	cag	gga	acc	cac	ggc	cga	ata	gcc	gtg	agc	cgg	576																							
Asn	Arg	Asn	Phe	Cys	Gln	Gly	Thr	His	Gly	Arg	Ile	Ala	Val	Ser	Arg																								
180										185										190																			
aat	cct	gca	cgg	tgc	cac	ctc	cac	aca	cac	cta	aca	tat	gcc	tgc	ctg	624																							
Asn	Pro	Ala	Arg	Cys	His	Leu	His	Thr	His	Leu	Thr	Tyr	Ala	Cys	Leu																								
195										200										205																			
atc	tgaccaaacac atgctcgcca ccctcaccac acacc															662																							
Ile																																							
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Ala	Ser	Thr	Cys	Ala	Trp	Pro	Gly	Phe	Pro	Gly	Gly	Gly	Gly	Lys	Val																								
1				5					10					15																									
Gly	Xaa	Met	Arg	Met	Pro	Cys	Pro	Thr	Met	Pro	Ser	Trp	Ser	Ser	Thr																								
20										25										30																			
Lys	Arg	Xaa	Ala	Gln	Trp	Gln	Thr	Gly	Cys	Thr	Thr	Ser	Phe	Gly	Gly																								
35										40										45																			
Ser	Trp	Arg	Ser	Ala	Val	Gly	Ala	Gly	His	Ser	Ala	Cys	Ala	Trp	Arg																								
50										55										60																			
Asn	Ala	Thr	Gly	Cys	Leu	Ala	Lys	Pro	Ser	Leu	Arg	Thr	Cys	Gly	Pro																								
65										70										75										80									
Arg	Ser	Met	Ala	Ala	Ala	Arg	Arg	Cys	Leu	Cys	Trp	Pro	Thr	Arg	Thr																								
85										90										95																			



Gly Ser Val Val Ser Cys Ala Pro Xaa Xaa Leu Leu Ala Gln Gln Arg  
100 105 110

Leu Leu Xaa Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Xaa Pro  
115 120 125

Asp Gly Gln Ala Ser Arg Leu Xaa Asp Ala Leu Thr Ser Ala Ser Ala  
130 135 140

Ala Arg Val Ser Ser Ser Gly Pro Thr Ser Pro Val Val Ala Gln Leu  
145 150 155 160

Leu Arg Pro Ala Cys Met Ala Leu Thr Arg Asp Asn His His Phe Tyr  
165 170 175

Asn Arg Asn Phe Cys Gln Gly Thr His Gly Arg Ile Ala Val Ser Arg  
180 185 190

Asn Pro Ala Arg Cys His Leu His Thr His Leu Thr Tyr Ala Cys Leu  
195 200 205

Ile

<210> 25

<211> 4865

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (107)..(2617)

<220>

<221> mat\_peptide

<222> (173)..(2617)

<220>

<221> misc\_feature

<222> (189)

<223> Xaa translation depends on genetic code

<400> 25

aaataactcc cttgcctcaa aaactgctcg gtcaaacggt gatagcaaac caccgattca 60

caggggccact gctgctcaca naascagtga ggatgatgcc aggatg atg tct gcc 115  
Met Ser Ala

-20

tcg	cgc	ctg	gct	ggg	act	ctg	atc	cca	gcc	atg	gcc	ttc	ctc	tcc	tgc	163
Ser	Arg	Leu	Ala	Gly	Thr	Leu	Ile	Pro	Ala	Met	Ala	Phe	Leu	Ser	Cys	
				-15					-10					-5		
gtg	aga	cca	gaa	agc	tgg	gag	ccc	tgc	gtg	gag	gtt	cct	aat	att	act	211
Val	Arg	Pro	Glu	Ser	Trp	Glu	Pro	Cys	Val	Glu	Val	Pro	Asn	Ile	Thr	
		-1	1				5					10				
tat	caa	tgc	atg	gag	ctg	aat	ttc	tac	aaa	atc	ccc	gac	aac	ctc	ccc	259
Tyr	Gln	Cys	Met	Glu	Leu	Asn	Phe	Tyr	Lys	Ile	Pro	Asp	Asn	Leu	Pro	
	15					20					25					
ttc	tca	acc	aag	aac	ctg	gac	ctg	agc	ttt	aat	ccc	ctg	agg	cat	tta	307
Phe	Ser	Thr	Lys	Asn	Leu	Asp	Leu	Ser	Phe	Asn	Pro	Leu	Arg	His	Leu	
	30				35					40					45	
ggc	agc	tat	agc	ttc	ttc	agt	ttc	cca	gaa	ctg	cag	gtg	ctg	gat	tta	355
Gly	Ser	Tyr	Ser	Phe	Phe	Ser	Phe	Pro	Glu	Leu	Gln	Val	Leu	Asp	Leu	
				50					55					60		
tcc	agg	tgt	gaa	atc	cag	aca	att	gaa	gat	ggg	gca	tat	cag	agc	cta	403
Ser	Arg	Cys	Glu	Ile	Gln	Thr	Ile	Glu	Asp	Gly	Ala	Tyr	Gln	Ser	Leu	
			65					70					75			
agc	cac	ctc	tct	acc	tta	ata	ttg	aca	gga	aac	ccc	atc	cag	agt	tta	451
Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Thr	Gly	Asn	Pro	Ile	Gln	Ser	Leu	
		80					85					90				
gcc	ctg	gga	gcc	ttt	tct	gga	cta	tca	agt	tta	cag	aag	ctg	gtg	gct	499
Ala	Leu	Gly	Ala	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Lys	Leu	Val	Ala	
		95				100					105					
gtg	gag	aca	aat	cta	gca	tct	cta	gag	aac	ttc	ccc	att	gga	cat	ctc	547
Val	Glu	Thr	Asn	Leu	Ala	Ser	Leu	Glu	Asn	Phe	Pro	Ile	Gly	His	Leu	
	110				115					120				125		
aaa	act	ttg	aaa	gaa	ctt	aat	gtg	gct	cac	aat	ctt	atc	caa	tct	ttc	595
Lys	Thr	Leu	Lys	Glu	Leu	Asn	Val	Ala	His	Asn	Leu	Ile	Gln	Ser	Phe	
				130					135					140		
aaa	tta	cct	gag	tat	ttt	tct	aat	ctg	acc	aat	cta	gag	cac	ttg	gac	643
Lys	Leu	Pro	Glu	Tyr	Phe	Ser	Asn	Leu	Thr	Asn	Leu	Glu	His	Leu	Asp	
			145					150					155			
ctt	tcc	agc	aac	aag	att	caa	agt	att	tat	tgc	aca	gac	ttg	cgg	gtt	691
Leu	Ser	Ser	Asn	Lys	Ile	Gln	Ser	Ile	Tyr	Cys	Thr	Asp	Leu	Arg	Val	
			160				165					170				
cta	cat	caa	atg	ccc	cta	ctc	aat	ctc	tct	tta	gac	ctg	tcc	ctg	aay	739
Leu	His	Gln	Met	Pro	Leu	Leu	Asn	Leu	Ser	Leu	Asp	Leu	Ser	Leu	Xaa	
	175					180					185					

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Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His	
190 195 200 205	
aag ctg act tta aga aat aat ttt gat agt tta aat gta atg aaa act	835
Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser 215 Leu Asn Val Met Lys 220 Thr	
210 220	
tgt att caa ggt ctg gct ggt tta gaa gtc cat cgt ttg gtt ctg gga	883
Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly	
225 230 235	
gaa ttt aga aat gaa gga aac ttg gaa aag ttt gac aaa tct gct cta	931
Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu	
240 245 250	
gag ggc ctg tgc aat ttg acc att gaa gaa ttc cga tta gca tac tta	979
Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu	
255 260 265	
gac tac tac ctc gat gat att att gac tta ttt aat tgt ttg aca aat	1027
Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn	
270 275 280 285	
gtt tct tca ttt tcc ctg gtg agt gtg act att gaa agg gta aaa gac	1075
Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp	
290 295 300	
ttt tct tat aat ttc gga tgg caa cat tta gaa tta gtt aac tgt aaa	1123
Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys	
305 310 315	
ttt gga cag ttt ccc aca ttg aaa ctc aaa tct ctc aaa agg ctt act	1171
Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr	
320 325 330	
ttc act tcc aac aaa ggt ggg aat gct ttt tca gaa gtt gat cta cca	1219
Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro	
335 340 345	
agc ctt gag ttt cta gat ctc agt aga aat ggc ttg agt ttc aaa ggt	1267
Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly	
350 355 360 365	
tgc tgt tct caa agt gat ttt ggg aca acc agc cta aag tat tta gat	1315
Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp	
370 375 380	
ctg agc ttc aat ggt gtt att acc atg agt tca aac ttc ttg ggc tta	1363
Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu	
385 390 395	
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Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met	

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aat	aag	acc	atc	att	ggc	gtg	tcg	gtc	ctc	agt	gtg	ctt	gta	gta	tct	2035																								
Asn	Lys	Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser																									
610										615										620																				

ggt gta gca gtt ctg gtc tat aag ttc tat ttt cac ctg atg ctt ctt	2083
Val Val Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu	
625 630 635	
gct ggc tgc ata aag tat ggt aga ggt gaa aac atc tat gat gcc ttt	2131
Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe	
640 645 650	
ggt atc tac tca agc cag gat gag gac tgg gta agg aat gag cta gta	2179
Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val	
655 660 665	
aag aat tta gaa gaa ggg gtg cct cca ttt cag ctc tgc ctt cac tac	2227
Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr	
670 675 680 685	
aga gac ttt att ccc ggt gtg gcc att gct gcc aac atc atc cat gaa	2275
Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Asn Ile Ile His Glu	
690 695 700	
ggt ttc cat aaa agc cga aag gtg att gtt gtg gtg tcc cag cac ttc	2323
Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe	
705 710 715	
atc cag agc cgc tgg tgt atc ttt gaa tat gag att gct cag acc tgg	2371
Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp	
720 725 730	
cag ttt ctg agc agt cgt gct ggt atc atc ttc att gtc ctg cag aag	2419
Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys	
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gct gag aag acc ctg ctc agg cag cag gtg gag ctg tac cgc ctt ctc	2467
Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Tyr Arg Leu Leu	
750 755 760 765	
agc agg aac act tac ctg gag tgg gag gac agt gtc ctg ggg cgg cac	2515
Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His	
770 775 780	
atc ttc tgg aga cga ctc aga aaa gcc ctg ctg gat ggt aaa tca tgg	2563
Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp	
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aat cca gaa gga aca gtg ggt aca gga tgc aat tgg cag gaa gca aca	2611
Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr	
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tct atc tgaagaggaa aaataaaaac ctctgaggc atttcttgcc cagctgggctc	2667
Ser Ile	
815	
caacacttgt tcagttaata agtattaata gctgccacat gtcaggcctt atgctaaggg	2727

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<211> 837

<212> PRT

<213> Unknown

<400> 26

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Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp  
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Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu  
 30 35 40

Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu Leu Gln Val  
 45 50 55

Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr  
 60 65 70

Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile  
 75 80 85 90

Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys  
 95 100 105

Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile  
 110 115 120

Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile  
 125 130 135

Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu  
 140 145 150

His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp  
 155 160 165 170

Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu  
 175 180 185

Ser Leu Xaa Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile  
 190 195 200

Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val  
 205 210 215

Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu  
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Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys  
 235 240 245 250

Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu  
 255 260 265

Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys  
 270 275 280

Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg  
 285 290 295

Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val  
 300 305 310

Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys  
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Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val  
 335 340 345

Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser  
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Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys  
 365 370 375

Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe  
 380 385 390

Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu  
 395 400 405 410



Lys	Gln	Met	Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile
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Tyr	Leu	Asp	Ile	Ser	His	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile
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Phe	Asn	Gly	Leu	Ser	Ser	Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser
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Phe	Gln	Glu	Asn	Phe	Leu	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu
	460					465					470				
Thr	Phe	Leu	Asp	Leu	Ser	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr
475					480					485					490
Ala	Phe	Asn	Ser	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn
				495					500					505	
Asn	Phe	Phe	Ser	Leu	Asp	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu
			510					515					520		
Gln	Val	Leu	Asp	Tyr	Ser	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln
		525					530					535			
Glu	Leu	Gln	His	Phe	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln
	540					545					550				
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Lys	Asp	Gln	Arg	Gln	Leu	Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala
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Thr	Pro	Ser	Asp	Lys	Gln	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr
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Cys	Gln	Met	Asn	Lys	Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu
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Val	Val	Ser	Val	Val	Ala	Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu
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Met	Leu	Leu	Ala	Gly	Cys	Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr
635					640					645					650
Asp	Ala	Phe	Val	Ile	Tyr	Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn
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Glu	Leu	Val	Lys	Asn	Leu	Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys
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Leu	His	Tyr	Arg	Asp	Phe	Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile
		685					690					695			

Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser  
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Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala  
715 720 725 730

Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val  
735 740 745

Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr  
750 755 760

Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu  
765 770 775

Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly  
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Glu Ala Thr Ser Ile  
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<211> 300

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised  
Mus musculus

<220>

<221> CDS

<222> (1)..(300)

<220>

<221> misc\_feature

<222> (62)..(100)

<223> Xaa translation depends on genetic code

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gtt ctc tca cta aaa gat aac aat gtc aca gct gtc ccc acc act ttg 96  
Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu  
20 25 30

cca cct aat tta cta gag ctc tat ctt tat aac aat atc att aag aaa	144
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
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atc caa gaa aat gat ttc aat aac ctc aat gag ttg caa gtn ctt gac	192
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
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cta ngt gga aat tgc cct cga tgt nat aat gtc cca tat ccg tgt aca	240
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
ccg tgt gaa aat aat tcc ccc tta cag atc cat gan aat gct ttc aat	288
Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Xaa Asn Ala Phe Asn	
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tca tcg aca gan	300
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Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
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Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
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Ser Ser Thr Xaa	
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 <212> DNA  
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<223> Description of Unknown Organism:rodent; surmised  
Mus musculus

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<222> (1)..(1182)

<400> 29

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atg	ccg	cca	aat	cta	aag	aat	ctc	tcc	ttg	gcc	aaa	aat	ggg	ctc	aaa	96
Met	Pro	Pro	Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	
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tct	ttc	ttt	tgg	gac	aga	ctc	cag	tta	ctg	aag	cat	ttg	gaa	att	ttg	144
Ser	Phe	Phe	Trp	Asp	Arg	Leu	Gln	Leu	Leu	Lys	His	Leu	Glu	Ile	Leu	
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gac	ctc	agc	cat	aac	cag	ctg	aca	aaa	gta	cct	gag	aga	ttg	gcc	aac	192
Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Lys	Val	Pro	Glu	Arg	Leu	Ala	Asn	
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tgt	tcc	aaa	agt	ctc	aca	aca	ctg	att	ctt	aag	cat	aat	caa	atc	agg	240
Cys	Ser	Lys	Ser	Leu	Thr	Thr	Leu	Ile	Leu	Lys	His	Asn	Gln	Ile	Arg	
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caa	ttg	aca	aaa	tat	ttt	cta	gaa	gat	gct	ttg	caa	ttg	cgc	tat	cta	288
Gln	Leu	Thr	Lys	Tyr	Phe	Leu	Glu	Asp	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	
				85					90					95		

gac	atc	agt	tca	aat	aaa	atc	cag	gtc	att	cag	aag	act	agc	ttc	cca	336
Asp	Ile	Ser	Ser	Asn	Lys	Ile	Gln	Val	Ile	Gln	Lys	Thr	Ser	Phe	Pro	
			100					105					110			

gaa	aat	gtc	ctc	aac	aat	ctg	gag	atg	ttg	gtt	tta	cat	cac	aat	cgc	384
Glu	Asn	Val	Leu	Asn	Asn	Leu	Glu	Met	Leu	Val	Leu	His	His	Asn	Arg	
		115					120					125				

ttt	ctt	tgc	aac	tgt	gat	gct	gtg	tgg	ttt	gtc	tgg	tgg	gtt	aac	cat	432
Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Val	Val	Asn	His	
		130				135					140					

aca	gat	gtt	act	att	cca	tac	ctg	gcc	act	gat	gtg	act	tgt	gta	ggt	480
Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly	
145					150					155					160	

cca	gga	gca	cac	aaa	ggg	caa	agt	gtc	ata	tcc	ctt	gat	ctg	tat	acg	528
Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr	
				165					170					175		

tgt	gag	tta	gat	ctc	aca	aac	ctg	att	ctg	ttc	tca	ggt	tcc	ata	tca	576
Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Val	Ser	Ile	Ser	
			180					185					190			
tca	gtc	ctc	ttt	ctt	atg	gta	ggt	atg	aca	aca	agt	cac	ctc	ttt	ttc	624
Ser	Val	Leu	Phe	Leu	Met	Val	Val	Met	Thr	Thr	Ser	His	Leu	Phe	Phe	
			195				200					205				
tgg	gat	atg	tgg	tac	att	tat	tat	ttt	tgg	aaa	gca	aag	ata	aag	ggg	672
Trp	Asp	Met	Trp	Tyr	Ile	Tyr	Tyr	Phe	Trp	Lys	Ala	Lys	Ile	Lys	Gly	
	210					215					220					
tat	cca	gca	tct	gca	atc	cca	tgg	agt	cct	tgt	tat	gat	gct	ttt	att	720
Tyr	Pro	Ala	Ser	Ala	Ile	Pro	Trp	Ser	Pro	Cys	Tyr	Asp	Ala	Phe	Ile	
225					230					235					240	
gtg	tat	gac	act	aaa	aac	tca	gct	gtg	aca	gaa	tgg	ggt	ttg	cag	gag	768
Val	Tyr	Asp	Thr	Lys	Asn	Ser	Ala	Val	Thr	Glu	Trp	Val	Leu	Gln	Glu	
				245					250					255		
ctg	gtg	gca	aaa	ttg	gaa	gat	cca	aga	gaa	aaa	cac	ttc	aat	ttg	tgt	816
Leu	Val	Ala	Lys	Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	
			260					265						270		
cta	gaa	gaa	aga	gac	tgg	cta	cca	gga	cag	cca	ggt	cta	gaa	aac	ctt	864
Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	
			275				280					285				
tcc	cag	agc	ata	cag	ctc	agc	aaa	aag	aca	gtg	ttt	gtg	atg	aca	cag	912
Ser	Gln	Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Gln	
	290					295					300					
aaa	tat	gct	aag	act	gag	agt	ttt	aag	atg	gca	ttt	tat	ttg	tct	cat	960
Lys	Tyr	Ala	Lys	Thr	Glu	Ser	Phe	Lys	Met	Ala	Phe	Tyr	Leu	Ser	His	
305					310					315					320	
cag	agg	ctc	ctg	gat	gaa	aaa	gtg	gat	gtg	att	atc	ttg	ata	ttc	ttg	1008
Gln	Arg	Leu	Leu	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	Leu	
				325					330					335		
gaa	aga	cct	ctt	cag	aag	tct	aag	ttt	ctt	cag	ctc	agg	aag	aga	ctc	1056
Glu	Arg	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	Leu	
			340					345					350			
tgc	agg	agc	tct	gtc	ctt	gag	tgg	cct	gca	aat	cca	cag	gct	cac	cca	1104
Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	Pro	
		355					360					365				
tac	ttc	tgg	cag	tgc	ctg	aaa	aat	gcc	ctg	acc	aca	gac	aat	cat	gtg	1152
Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	Val	
		370				375					380					
gct	tat	agt	caa	atg	ttc	aag	gaa	aca	gtc	tagctctctg	aagaatgtca					1202
Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val							

385

390

ccacctagga catgccttgg tacctgaagt ttccataaag gtttccataa atgaaggctct 1262  
 gaatttttcc taacagttgt catggctcag attgggtggga aatcatcaat atatggctaa 1322  
 gaaattaaga aggggagact gatagaagat aatttctttc ttcattgtgcc atgctcagtt 1382  
 aaatatttcc cctagctcaa atctgaaaaa ctgtgcctag gagacaacac aaggctttga 1442  
 tttatctgca tacaattgat aagagccaca catctgccct gaagaagtac tagtagtttt 1502  
 agtagtaggg taaaaattac acaagctttc tctctctctg atactgaact gtaccagagt 1562  
 tcaatgaaat aaaagcccag agaacttctc agtaaattgt ttcattatca tgtagtatcc 1622  
 accatgcaat atgccacaaa rccgctactg gtacaggaca gntggtagct gcttcaakgc 1682  
 ctcttatcat tttcttgggg cccatggagg ggttctytgg gaaadagga agkttttttt 1742  
 tggccatcca tgaa 1756

&lt;210&gt; 30

&lt;211&gt; 394

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;400&gt; 30

Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly  
 1 5 10 15

Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys  
 20 25 30

Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu  
 35 40 45

Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn  
 50 55 60

Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg  
 65 70 75 80

Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu  
 85 90 95

Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro  
 100 105 110

Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg  
 115 120 125

Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His
130						135					140				
Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly
145					150					155					160
Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr
				165					170					175	
Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Val	Ser	Ile	Ser
			180					185					190		
Ser	Val	Leu	Phe	Leu	Met	Val	Val	Met	Thr	Thr	Ser	His	Leu	Phe	Phe
		195					200					205			
Trp	Asp	Met	Trp	Tyr	Ile	Tyr	Tyr	Phe	Trp	Lys	Ala	Lys	Ile	Lys	Gly
	210					215					220				
Tyr	Pro	Ala	Ser	Ala	Ile	Pro	Trp	Ser	Pro	Cys	Tyr	Asp	Ala	Phe	Ile
225					230					235					240
Val	Tyr	Asp	Thr	Lys	Asn	Ser	Ala	Val	Thr	Glu	Trp	Val	Leu	Gln	Glu
				245					250					255	
Leu	Val	Ala	Lys	Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys
			260					265					270		
Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu
		275					280					285			
Ser	Gln	Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Gln
	290					295					300				
Lys	Tyr	Ala	Lys	Thr	Glu	Ser	Phe	Lys	Met	Ala	Phe	Tyr	Leu	Ser	His
305					310					315					320
Gln	Arg	Leu	Leu	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	Leu
				325					330					335	
Glu	Arg	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	Leu
			340					345					350		
Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	Pro
		355					360					365			
Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	Val
370						375					380				
Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
385					390										

<210> 31  
<211> 999

<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>  
<221> CDS  
<222> (2)..(847)

<220>  
<221> misc\_feature  
<222> (1)..(282)  
<223> Xaa translation depends on genetic code

<400> 31  
c tcn gat gcc aag att cgg cac nag gca tat tca gag gtc atg atg gtt 49  
Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val  
1 5 10 15  
gga tgg tca gat tca tac acc tgt gaa tac cct tta aac cta agg gga 97  
Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly  
20 25 30  
act agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct 145  
Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala  
35 40 45  
ctg ttg att gtc acc att gtg gtt att atg cta gtt ctg ggg ttg gct 193  
Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala  
50 55 60  
gtg gcc ttc tgc tgt ctc cac ttt gat ctg ccc tgg tat ctc agg atg 241  
Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met  
65 70 75 80  
cta ggt caa tgc aca caa aca tgg cac agg gtt agg aaa aca acc caa 289  
Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln  
85 90 95  
gaa caa ctc aag aga aat gtc cga ttc cac gca ttt att tca tac agt 337  
Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser  
100 105 110  
gaa cat gat tct ctg tgg gtg aag aat gaa ttg atc ccc aat cta gag 385  
Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu  
115 120 125  
aag gaa gat ggt tct atc ttg att tgc ctt tat gaa agc tac ttt gac 433  
Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp  
130 135 140



cct ggc aaa agc att agt gaa aat att gta agc ttc att gag aaa agc	481
Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser	
145 150 155 160	
tat aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag aat gag tgg	529
Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp	
165 170 175	
tgc cat tat gaa ttc tac ttt gcc cac cac aat ctc ttc cat gaa aat	577
Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn	
180 185 190	
tct gat cac ata att ctt atc tta ctg gaa ccc att cca ttc tat tgc	625
Ser Asp His Ile Ile Leu Ile Leu Glu Pro Ile Pro Phe Tyr Cys	
195 200 205	
att ccc acc agg tat cat aaa ctg raa gct ctc ctg gaa aaa aaa gca	673
Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Glu Lys Lys Ala	
210 215 220	
tac ttg gaa tgg ccc aag gat agg cgt aaa tgt ggg ctt tty tgg gca	721
Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala	
225 230 235 240	
aat ctt cga gct gct gtt aat gtt aat gta tta gcc acc aga gaa atg	769
Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met	
245 250 255	
tat gaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct	817
Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser	
260 265 270	
aca atc tyt ctg atg aga aca gac tgt yta taaaatccca cagtccttgg	867
Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa	
275 280	
gaagttgggg accacataca ctgttgggat gtacattgat acaaccttta tgatggcaat	927
ttgacaatat ttattaaaaat aaaaaatggt tattcccttc aaaaaaaaaa aaaaaaaaaa	987
aaaaaaaaaa aa	999

<210> 32

<211> 282

<212> PRT

<213> Unknown

<400> 32

Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val
1 5 10 15

Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly
20 25 30

Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala  
 35 40 45  
 Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala  
 50 55 60  
 Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met  
 65 70 75 80  
 Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln  
 85 90 95  
 Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser  
 100 105 110  
 Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu  
 115 120 125  
 Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp  
 130 135 140  
 Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser  
 145 150 155 160  
 Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp  
 165 170 175  
 Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn  
 180 185 190  
 Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys  
 195 200 205  
 Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Leu Glu Lys Lys Ala  
 210 215 220  
 Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala  
 225 230 235 240  
 Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met  
 245 250 255  
 Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser  
 260 265 270  
 Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa  
 275 280

<210> 33  
 <211> 1173  
 <212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(1008)

<220>

<221> misc\_feature

<222> (285)

<223> Xaa translation depends on genetic code

<400> 33

ctg	cct	gct	ggc	acc	cgg	ctc	cgg	agg	ctg	gat	gtc	agc	tgc	aac	agc	48
Leu	Pro	Ala	Gly	Thr	Arg	Leu	Arg	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	
1				5				10						15		

atc	agc	ttc	gtg	gcc	ccc	ggc	ttc	ttt	tcc	aag	gcc	aag	gag	ctg	cga	96
Ile	Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	
			20					25					30			

gag	ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	aca	gtg	gac	cac	tcc	tgg	144
Glu	Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	Thr	Val	Asp	His	Ser	Trp	
		35				40					45					

ttt	ggg	ccc	ctg	gcg	agt	gcc	ctg	caa	ata	cta	gat	gta	agc	gcc	aac	192
Phe	Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	
		50				55					60					

cct	ctg	cac	tgc	gcc	tgt	ggg	gcg	gcc	ttt	atg	gac	ttc	ctg	ctg	gag	240
Pro	Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	
65					70				75					80		

gtg	cag	gct	gcc	gtg	ccc	ggt	ctg	ccc	agc	cgg	gtg	aag	tgt	ggc	agt	288
Val	Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	
				85					90					95		

ccg	ggc	cag	ctc	cag	ggc	ctc	agc	atc	ttt	gca	cag	gac	ctg	cgc	ctc	336
Pro	Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	
			100					105					110			

tgc	ctg	gat	gag	gcc	ctc	tcc	tgg	gac	tgt	ttc	gcc	ctc	tgc	ctg	ctg	384
Cys	Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	
		115					120						125			

gct	gtg	gct	ctg	ggc	ctg	ggt	gtg	ccc	atg	ctg	cat	cac	ctc	tgt	ggc	432
Ala	Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	
		130				135						140				

tgg	gac	ctc	tgg	tac	tgc	ttc	cac	ctg	tgc	ctg	gcc	tgg	ctt	ccc	tgg	480
Trp	Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	

145		150		155		160	
cgg ggg cgg caa agt ggg cga gat gag gat gcc ctg ccc tac gat gcc		arg gly arg gln ser gly arg asp glu asp ala leu pro tyr asp ala	528				
		165		170		175	
ttc gtg gtc ttc gac aaa acg cag agc gca gtg gca gac tgg gtg tac		phe val val phe asp lys thr gln ser ala val ala asp trp val tyr	576				
		180		185		190	
aac gag ctt cgg ggg cag ctg gag gag tgc cgt ggg cgc tgg gca ctc		asn glu leu arg gly gln leu glu glu cys arg gly arg trp ala leu	624				
		195		200		205	
cgc ctg tgc ctg gag gaa cgc gac tgg ctg cct gcc aaa acc ctc ttt		arg leu cys leu glu glu arg asp trp leu pro gly lys thr leu phe	672				
		210		215		220	
gag aac ctg tgg gcc tcg gtc tat ggc agc cgc aag acg ctg ttt gtg		glu asn leu trp ala ser val tyr gly ser arg lys thr leu phe val	720				
		225		230		235	
ctg gcc cac acg gac cgg gtc agt ggt ctc ttg cgc gcc agc ttc ctg		leu ala his thr asp arg val ser gly leu leu arg ala ser phe leu	768				
		245		250		255	
ctg gcc cag cag cgc ctg ctg gag gac cgc aag gac gtc gtg gtg ctg		leu ala gln gln arg leu leu glu asp arg lys asp val val val leu	816				
		260		265		270	
gtg atc ctg agc cct gac ggc cgc cgc tcc cgc tac gkg cgg ctg cgc		val ile leu ser pro asp gly arg arg ser arg tyr xaa arg leu arg	864				
		275		280		285	
cag cgc ctc tgc cgc cag agt gtc ctc ctc tgg ccc cac cag ccc agt		gln arg leu cys arg gln ser val leu leu trp pro his gln pro ser	912				
		290		295		300	
ggt cag cgc agc ttc tgg gcc cag ctg ggc atg gcc ctg acc agg gac		gly gln arg ser phe trp ala gln leu gly met ala leu thr arg asp	960				
		310		315		320	
aac cac cac ttc tat aac cgg aac ttc tgc cag gga ccc acg gcc gaa		asn his his phe tyr asn arg asn phe cys gln gly pro thr ala glu	1008				
		325		330		335	
tagccgtgag ccggaatcct gcacgggtgcc acctccacac tcacctcacc tctgctgtgcc			1068				
tggtctgacc ctcccctgct gcctccctc accccacacc tgacacagag caggcactca			1128				
ataaatgcta ccgaaggcta aaaaaaaaaa aaaaaaaaaa aanna			1173				

<210> 34  
<211> 336  
<212> PRT  
<213> Unknown

<400> 34

Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser  
1 5 10 15

Ile Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg  
20 25 30

Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp  
35 40 45

Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn  
50 55 60

Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu  
65 70 75 80

Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser  
85 90 95

Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu  
100 105 110

Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu  
115 120 125

Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly  
130 135 140

Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp  
145 150 155 160

Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala  
165 170 175

Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr  
180 185 190

Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu  
195 200 205

Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe  
210 215 220

Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val  
225 230 235 240

Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu  
245 250 255

Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu  
 260 265 270  
 Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg  
 275 280 285  
 Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser  
 290 295 300  
 Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp  
 305 310 315 320  
 Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu  
 325 330 335

<210> 35

<211> 497

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised  
Mus musculus

<400> 35

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 cgtcccgcta tgtgcgactg cgccagcgtc tctgcccga gagtgtgctc ttctggcccc 180  
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 accgccactt ctataaccag aacttctgcc ggggacctac agcagaatag ctcagagcaa 300  
 cagctggaaa cagctgcctc ttcattgtctg gttcccagag tgctctgcct gccttgctct 360  
 gtcttactac accgctattt ggcaagtgcg caatatatgc taccaagcca ccaggccac 420  
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<210> 36

<211> 3099

<212> DNA

<213> Unknown

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<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

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 <223> Xaa translation depends on genetic code

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 gcc gaa gaa aat ttt tct aga agc tat cct tgt gat gag aaa aag caa 96  
 Ala Glu Glu Asn Phe Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln  
 -1 1 5 10 15  
 aat gac tca gtt att gca gag tgc agc aat cgt cga cta cag gaa gtt 144  
 Asn Asp Ser Val Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val  
 20 25 30  
 cca caa acg gtg ggc aaa tat gtg aca gaa cta gac ctg tct gat aat 192  
 Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn  
 35 40 45  
 ttc atc aca cac ata acg aat gaa tca ttt caa ggg ctg caa aat ctc 240  
 Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu  
 50 55 60  
 act aaa ata aat cta aac cac aac ccc aat gta cag cac cag aac gga 288  
 Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly  
 65 70 75  
 aat ccc ggt ata caa tca aat ggc ttg aat atc aca gac ggg gca ttc 336  
 Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe  
 80 85 90 95  
 ctc aac cta aaa aac cta agg gag tta ctg ctt gaa gac aac cag tta 384  
 Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Glu Asp Asn Gln Leu  
 100 105 110  
 ccc caa ata ccc tct ggt ttg cca gag tct ttg aca gaa ctt agt cta 432  
 Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu  
 115 120 125  
 att caa aac aat ata tac aac ata act aaa gag ggc att tca aga ctt 480  
 Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu  
 130 135 140

aa	aac	ttg	aaa	aat	ctc	tat	ttg	gcc	tg	aac	tg	tat	ttt	aac	aaa	528
le	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn	Cys	Tyr	Phe	Asn	Lys	
	145					150					155					
tt	tg	gag	aaa	act	aac	ata	gaa	gat	gga	gta	ttt	gaa	acg	ctg	aca	576
al	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly	Val	Phe	Glu	Thr	Leu	Thr	
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at	ttg	gag	ttg	cta	tca	cta	tct	ttc	aat	tct	ctt	tca	cat	gtg	cca	624
sn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe	Asn	Ser	Leu	Ser	His	Val	Pro	
				180					185					190		
cc	aaa	ctg	cca	agc	tcc	cta	cgc	aaa	ctt	ttt	ctg	agc	aac	acc	cag	672
ro	Lys	Leu	Pro	Ser	Ser	Leu	Arg	Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	
			195					200					205			
atc	aaa	tac	att	agt	gaa	gaa	gat	ttc	aag	gga	ttg	ata	aat	tta	aca	720
ile	Lys	Tyr	Ile	Ser	Glu	Glu	Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	
	210						215					220				
tta	cta	gat	tta	agc	ggg	aac	tgt	cgc	agg	tg	ttc	aat	gcc	cca	ttt	768
Leu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	
	225					230					235					
cca	ggc	gtg	cct	tgt	gat	ggg	ggt	gct	tca	att	aat	ata	gat	cgt	ttt	816
Pro	Cys	Val	Pro	Cys	Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	
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gct	ttt	caa	aac	ttg	acc	caa	ctt	cga	tac	cta	aac	ctc	tct	agc	act	864
Ala	Phe	Gln	Asn	Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	
				260					265					270		
tcc	ctc	agg	aag	att	aat	gct	gcc	tg	ttt	aaa	aat	atg	cct	cat	ctg	912
Ser	Leu	Arg	Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	
			275					280					285			
aag	gtg	ctg	gat	ctt	gaa	ttc	aac	tat	tta	gtg	gga	gaa	ata	gcc	tct	960
Lys	Val	Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Ala	Ser	
		290					295					300				
ggg	gca	ttt	tta	acg	atg	ctg	ccc	cgc	tta	gaa	ata	ctt	gac	ttg	tct	1008
Gly	Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser	
	305					310					315					
ttt	aac	tat	ata	aag	ggg	agt	tat	cca	cag	cat	att	aat	att	tcc	aga	1056
Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	Arg	
320					325					330				335		
aac	ttc	tct	aaa	ctt	ttg	tct	cta	cgg	gca	ttg	cat	tta	aga	ggg	tat	1104
Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	Gly	Tyr	
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g ttc cag gaa ctc aga gaa gat gat ttc cag ccc ctg atg cag ctt	1152
al Phe Gln 355 Leu Arg Glu Asp 360 Phe Gln Pro Leu Met Gln Leu	
ca aac tta tgc act atc aac ttg ggt att aat ttt att aag caa atc	1200
ro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe Ile Lys Gln Ile	
at ttc aaa ctt ttc caa aat ttc tcc aat ctg gaa att att tac ttg	1248
sp Phe 385 Lys Leu Phe Gln Asn 390 Phe Ser Asn Leu Gln Ile Ile Tyr Leu	
ca gaa aac aga ata tca ccg ttg gta aaa gat acc ccg cag agt tat	1296
er Glu Asn Arg Ile Ser Pro Leu Val Lys Asp 410 Thr Arg Gln Ser Tyr 415	
ca aat agt tcc tct ttt caa cgt cat atc ccg aaa cga cgc tca aca	1344
la Asn Ser Ser Ser Phe 420 Gln Arg His Ile Arg Lys Arg Arg Ser Thr 430	
gat ttt gag ttt gac cca cat tgc aac ttt tat cat ttc acc cgt cct	1392
asp Phe 435 Glu Phe Asp Pro His Ser Asn 440 Phe Tyr His Phe Thr Arg Pro 445	
tta ata aag cca caa tgt gct gct tat gga aaa gcc tta gat tta agc	1440
leu Ile 450 Lys Pro Gln Cys Ala Tyr Gly Lys Ala Leu Asp Leu Ser 460	
ctc aac agt att ttc ttc att ggg cca aac caa ttt gaa aat ctt cct	1488
leu Asn 465 Ser Ile Phe Phe Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro 475	
gac att gcc tgt tta aat ctg tct gca aat agc aat gct caa gtg tta	1536
asp Ile 480 Ala Cys Leu Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu 495	
agt gga act gaa ttt tca gcc att cct cat gtc aaa tat ttg gat ttg	1584
ser Gly Thr Glu Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu 510	
aca aac aat aga cta gac ttt gat aat gct agt gct ctt act gaa ttg	1632
thr Asn Asn Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu 525	
tcc gac ttg gaa gtt cta gat ctg agc tat aat tca cac tat ttc aga	1680
ser asp 530 leu glu val leu asp 535 leu ser tyr asn ser 540 his tyr phe arg	
ata gca ggc gta aca cat cat cta gaa ttt att caa aat ttc aca aat	1728
ile ala gly val thr his 550 his leu glu phe ile 555 gln asn phe thr asn 555	
cta aaa gtt tta aac ttg agc cac aac aac att tat act tta aca gat	1776
leu lys val leu asn leu ser his asn asn ile tyr thr leu thr asp	

560		565		570		575	
aag tat aac ctg gaa agc aag tcc ctg gta gaa tta gtt ttc agt ggc	1824						
Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly							
		580		585		590	
aat cgc ctt gac att ttg tgg aat gat gat gac aac agg tat atc tcc	1872						
Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asn Arg Tyr Ile Ser							
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att ttc aaa ggt ctc aag aat ctg aca cgt ctg gat tta tcc ctt aat	1920						
Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn							
		610		615		620	
agg ctc aag cac atc cca aat gaa gca ttc ctt aat ttg cca gcg agt	1968						
Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser							
		625		630		635	
ctc act gaa cta cat ata aat gat aat atg tta aag ttt ttt aac tgg	2016						
Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp							
		640		645		650	655
aca tta ctc cag cag ttt cct cgt ctc gag ttg ctt gac tta cgt gga	2064						
Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly							
		660		665		670	
aac aaa cta ctc ttt tta act gat agc cta tct gac ttt aca tct tcc	2112						
Asn Lys Leu Leu Phe Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser							
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ctt cgg aca ctg ctg ctg agt cat aac agg att tcc cac cta ccc tct	2160						
Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser							
		690		695		700	
ggc ttt ctt tct gaa gtc agt agt ctg aag cac ctc gat tta agt tcc	2208						
Gly Phe Leu Ser Glu Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser							
		705		710		715	
aat ctg cta aaa aca atm aac aaa tcc gca ctt gaa act aag acc acc	2256						
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Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr							
		740		745		750	
tgt gac att gga gat ttc cga aga tgg atg gat gaa cat ctg aat gtc	2352						
Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val							
		755		760		765	
aaa att ccc aga ctg gta gat gtc att tgt gcc agt cct ggg gat caa	2400						
Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln							
		770		775		780	

aga ggg aag agt att gtg agt ctg gag cta aca act tgt gtt tca gat	2448
Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	
785 790 795	
gtc act gca gtg ata tta ttt ttc ttc acg ttc ttt atc acc acc atg	2496
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr Met	
800 805 810 815	
gtt atg ttg gct gcc ctg gct cac cat ttg ttt tac tgg gat gtt tgg	2544
Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp Val Trp	
820 825 830	
ttt ata tat aat gtg tgt tta gct aag tta aaa ggc tac agg tct ctt	2592
Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu	
835 840 845	
tcc aca tcc caa act ttc tat gat gct tac att tct tat gac acc aaa	2640
Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys	
850 855 860	
gat gcc tct gtt act gac tgg gtg ata aat gag ctg cgc tac cac ctt	2688
Asp Ala Ser Val Thr Asp Val Ile Asn Glu Leu Arg Tyr His Leu	
865 870 875	
gaa gag agc cga gac aaa aac gtt ctc ctt tgt cta gag gag agg gat	2736
Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp	
880 885 890 895	
tgg gac ccg gga ttg gcc atc atc gac aac ctc atg cag agc atc aac	2784
Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn	
900 905 910	
caa agc aag aaa aca gta ttt gtt tta acc aaa aaa tat gca aaa agc	2832
Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Gln Lys Ser	
915 920 925	
tgg aac ttt aaa aca gct ttt tac ttg gcc ttg cag agg cta atg ggt	2880
Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly	
930 935 940	
gag aac atg gat gtg att ata ttt atc ctg ctg gag cca gtg tta cag	2928
Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln	
945 950 955	
cat tct ccg tat ttg agg cta ccg cag ccg atc tgt aag agc tcc atc	2976
His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile	
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ctc cag tgg cct gac aac ccg aag gca gaa ggc ttg ttt tgg caa act	3024
Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr	
980 985 990	
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3099

210> 37  
 211> 1032  
 212> PRT  
 213> Unknown

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Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn  
 35 40 45

Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu  
 50 55 60

Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly  
 65 70 75

Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe  
 80 85 90 95

Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu  
 100 105 110

Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu  
 115 120 125

Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu  
 130 135 140

Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys  
 145 150 155

Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr  
 160 165 170 175

Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro  
 180 185 190

o' Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln  
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 le Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr  
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 su Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe  
 225 230 235  
 ro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe  
 40 245 250 255  
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 er Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu  
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 gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser  
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 Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe Ile Lys Gln Ile  
 370 375 380  
 Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu Ile Ile Tyr Leu  
 385 390 395  
 Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr Arg Gln Ser Tyr  
 400 405 410 415  
 Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys Arg Arg Ser Thr  
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 Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His Phe Thr Arg Pro  
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 Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala Leu Asp Leu Ser  
 450 455 460  
 Leu Asn Ser Ile Phe Phe Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro  
 465 470 475

Asp Ile Ala Cys Leu Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu  
 480 485 490 495  
 Ser Gly Thr Glu Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu  
 500 505 510  
 Thr Asn Asn Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu  
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 Ser Asp Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg  
 530 535 540  
 Ile Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn  
 545 550 555  
 Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr Asp  
 560 565 570 575  
 Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly  
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 Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser  
 595 600 605  
 Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn  
 610 615 620  
 Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser  
 625 630 635  
 Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp  
 640 645 650 655  
 Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly  
 660 665 670  
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 Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser  
 690 695 700  
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 Asn Leu Leu Lys Thr Xaa Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr  
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 Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr  
 740 745 750  
 Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val  
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Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln  
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 Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp  
 785 790 795  
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 820 825 830  
 Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu  
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 850 855 860  
 Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu  
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 Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp  
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 Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn  
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 Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser  
 915 920 925  
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly  
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 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln  
 945 950 955  
 His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile  
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<210> 38  
 <211> 3046  
 <212> DNA  
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220>  
223> Description of Unknown Organism:primate; surmised  
Homo sapiens

220>  
221> CDS  
222> (111)..(2543)

220>  
221> mat\_peptide  
222> (168)..(2543)

400> 38

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Met Arg

ctc atc aga aac att tac ata ttt tgt agt att gtt atg aca gca gag 164  
Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu  
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Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu Met Thr Asn Cys  
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Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr  
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acg aca ctg gat tta tcc tat aac ctc ctt ttt caa ctc cag agt tca 308  
Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Ser Ser  
35 40 45

gat ttt cat tct gtc tcc aaa ctg aga gtt ttg att cta tgc cat aac 356  
Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn  
50 55 60

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Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys Glu Leu  
65 70 75

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Leu Leu Ala Gly Leu Arg Tyr Leu Asp Phe Ser Phe Asn Asp Phe Asp  
100 105 110

acc atg cct atc tgt gag gaa gct ggc aac atg tca cac ctg gaa atc 548  
Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile



115								120				125								
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Ala	His	Leu	His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro					
		145				150					155									
cat	tat	gaa	gaa	ggt	agc	ctg	ccc	atc	tta	aac	aca	aca	aaa	ctg	cac	692				
His	Tyr	Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His					
		160			165					170				175						
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Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	Trp	Asp	Asp					
		225				230					235									
ctt	ttc	ctt	atc	tta	caa	ttt	ggt	tgg	cat	aca	tca	gtg	gaa	cac	ttt	932				
Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	Val	Glu	His	Phe					
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Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	Tyr	Leu	Asp	His	Asn					
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Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	Thr	Ile	Lys	Leu	Glu	His					
			275					280					285							
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Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	Gln	Asp	Lys	Ile	Tyr	Leu	Leu					
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ttg	acc	aaa	atg	gac	ata	gaa	aac	ctg	aca	ata	tca	aat	gca	caa	atg	1124				
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Phe Ala Asn Asn Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln	
340 345 350	
ctg cct cac ttg aaa act ctc att ttg aat ggc aat aaa ctg gag aca	1268
Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr	
355 360 365	
ctt tct tta gta agt tgc ttt gct aac aac aca ccc ttg gaa cac ttg	1316
Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu	
370 375 380	
gat ctg agt caa aat cta tta caa cat aaa aat gat gaa aat tgc tca	1364
Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser	
385 390 395	
tgg cca gaa act gtg gtc aat atg aat ctg tca tac aat aaa ttg tct	1412
Trp Pro Glu Thr Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser	
400 405 410 415	
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Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu	
420 425 430	
aat aat aac caa atc caa act gta cct aaa gag act att cat ctg atg	1508
Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met	
435 440 445	
gcc tta cga gaa cta aat att gca ttt aat ttt cta act gat ctc cct	1556
Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp Leu Pro	
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gga tgc agt cat ttc agt aga ctt tca gtt ctg aac att gaa atg aac	1604
Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn	
465 470 475	
ttc att ctc agc cca tct ctg gat ttt gtt cag agc tgc cag gaa gtt	1652
Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln Glu Val	
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Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu	
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Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met Val Gly	
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Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr	
530 535 540	
agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct ctg	1844

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Ala	Phe	Cys	Cys	Leu	His	Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu	
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Gly	Gln	Cys	Thr	Gln	Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu	
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Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn		685		
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Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe	Tyr	Cys	Ile	
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ccc	acc	agg	tat	cat	aaa	ctg	aaa	gct	ctc	ctg	gaa	aaa	aaa	gca	tac	2372
Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Lys	Ala	Tyr	
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jaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct aca 2516  
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 770 775 780

atc tct ctg atg aga aca gat tgt cta taaaatccca cagtccttgg 2563  
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 785 790

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Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln  
 30 35 40 45

Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys  
 50 55 60

His Asn Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys  
 65 70 75

Glu Leu Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr

80

85

90

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Phe	Asp	Thr	Met	Pro	Ile	Cys	Glu	Glu	Ala	Gly	Asn	Met	Ser	His	Leu
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Lys	Ile	Ala	His	Leu	His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr
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Asp	Gly	Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly
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Asn	Ala	Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	Trp
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Asp	Asp	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	Val	Glu
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His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	Thr	Ile	Lys	Leu
270					275					280					285
Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	Gln	Asp	Lys	Ile	Tyr
			290						295					300	
Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	Leu	Thr	Ile	Ser	Asn	Ala
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370

375

380

His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn  
385 390 395

Cys Ser Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys  
400 405 410

Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu  
415 420 425

Asp Leu Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His  
430 435 440 445

Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp  
450 455 460

Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu  
465 470 475

Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln  
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Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys  
495 500 505

Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met  
510 515 520 525

Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg  
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Gly Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr  
545 550 555

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Ala Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg  
575 580 585

Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr  
590 595 600 605

Gln Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr  
610 615 620

Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu  
625 630 635

Glu Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe  
640 645 650

Asp	Pro	Gly	Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys
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Ser	Tyr	Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu
670				675						680					685
Trp	Cys	His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu
				690					695					700	
Asn	Ser	Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe	Tyr
			705					710					715		
Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Lys
		720					725						730		
Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly	Leu	Phe	Trp
	735					740					745				
Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu	Ala	Thr	Arg	Glu
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Met	Tyr	Glu	Leu	Gln	Thr	Phe	Thr	Glu	Leu	Asn	Glu	Glu	Ser	Arg	Gly
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Thr Val Leu Arg Leu Ser His Asn Arg Ile Gln Leu Asp Leu Ser  
50 55 60

gtt ttc aag ttc aac cag gat tta gaa tat ttg gat tta tct cat aat 397  
Val Phe Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn  
65 70 75

cag ttg caa aag ata tcc tgc cat cct att gtg agt ttc agg cat tta 445  
Gln Leu Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu  
80 85 90 95

gat ttc tca ttc aat gat ttc aag gcc ctg ccc atc tgt aag gaa ttt 493  
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ggc aac tta tca caa ctg aat ttc ttg gga ttg agt gct atg aag ctg 541  
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Gln Lys Leu Asp Leu Leu Pro Ile Ala His Leu His Leu Ser Tyr Ile  
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ctt ctg gat tta aga aat tat tat ata aaa gaa aat gag aca gaa agt 637  
Leu Leu Asp Leu Arg Asn Tyr Tyr Ile Lys Glu Asn Glu Thr Glu Ser  
145 150 155

cta caa att ctg aat gca aaa acc ctt cac ctt gtt ttt cac cca act 685  
Leu Gln Ile Leu Asn Ala Lys Thr Leu His Leu Val Phe His Pro Thr  
160 165 170 175

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180

185

190

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ala	Pro	Ser	Thr	Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr	
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gat	agt	att	ttt	gaa	aaa	tgt	tcc	acg	tta	gtt	aaa	ttg	gag	aca	ctt	1213
asp	Ser	Ile	Phe	Glu	Lys	Cys	Ser	Thr	Leu	Val	Lys	Leu	Glu	Thr	Leu	
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ile	Leu	Gln	Lys	Asn	Gly	Leu	Lys	Asp	Leu	Phe	Lys	Val	Gly	Leu	Met	
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thr	Lys	Asp	Met	Pro	Ser	Leu	Glu	Ile	Leu	Asp	Val	Ser	Trp	Asn	Ser	
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leu	Glu	Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser	Ile	
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Ser	Ser	Leu	Ser	Val	Leu	Ile	Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	
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Gly	Asp	Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	
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Tyr	Lys	Cys	Asp	Tyr	Pro	Glu	Ser	Tyr	Arg	Gly	Ser	Pro	Leu	Lys	Asp	
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Phe	His	Met	Ser	Glu	Leu	Ser	Cys	Asn	Ile	Thr	Leu	Leu	Ile	Val	Thr	
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Ile	Gly	Ala	Thr	Met	Leu	Val	Leu	Ala	Val	Thr	Val	Thr	Ser	Leu	Cys	
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Ile	Tyr	Leu	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Val	Cys	Gln	Trp	Thr	
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Gln	Thr	Arg	Arg	Arg	Ala	Arg	Asn	Ile	Pro	Leu	Glu	Glu	Gln	Gln	Arg	
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Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His	Tyr	Glu	Leu	Tyr	Phe		
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Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn	Asn	Leu	Ile	Leu	Ile		
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Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro	Asn	Lys	Tyr	His	Lys		
		705				710					715						
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Glu	Phe	Ala	Val	Asp	Lys	Ser	Lys	Arg	Gly	Leu	Ile	His	Val	Pro	Lys
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Ala	Glu	Leu	Gln	Val	Ser	Asp	Met	Ser	Phe	Leu	Ser	Glu	Leu	Thr	Val
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Leu	Arg	Leu	Ser	His	Asn	Arg	Ile	Gln	Leu	Leu	Asp	Leu	Ser	Val	Phe
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Lys	Phe	Asn	Gln	Asp	Leu	Glu	Tyr	Leu	Asp	Leu	Ser	His	Asn	Gln	Leu
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Gln	Lys	Ile	Ser	Cys	His	Pro	Ile	Val	Ser	Phe	Arg	His	Leu	Asp	Leu
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Ser	Phe	Asn	Asp	Phe	Lys	Ala	Leu	Pro	Ile	Cys	Lys	Glu	Phe	Gly	Asn
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Asp	Leu	Arg	Asn	Tyr	Tyr	Ile	Lys	Glu	Asn	Glu	Thr	Glu	Ser	Leu	Gln
			150						155					160	
Ile	Leu	Asn	Ala	Lys	Thr	Leu	His	Leu	Val	Phe	His	Pro	Thr	Ser	Leu
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Phe	Ala	Ile	Gln	Val	Asn	Ile	Ser	Val	Asn	Thr	Leu	Gly	Cys	Leu	Gln
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Asn	His	Ile	Glu	Thr	Thr	Trp	Lys	Cys	Leu	Val	Arg	Val	Phe	Gln	Phe

230

235

240

Leu	Trp	Pro	Lys	Pro	Val	Glu	Tyr	Leu	Asn	Ile	Tyr	Asn	Leu	Thr	Ile
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Lys	Ala	Leu	Thr	Ile	Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu	Phe	Ser
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Thr	Ile	Ser	Asp	Thr	Pro	Phe	Ile	His	Met	Leu	Cys	Pro	His	Ala	Pro
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Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser	Ile	Val	Val
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Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	Lys	Ser
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Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	Asn	Val
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Leu	Ser	Val	Leu	Ile	Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	Ser	Ala
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Asp	Phe	Phe	Gln	Ser	Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp
			485						490				495		
Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	Asn	Ile
		500					505					510			
Asp	Gln	Val	Ser	Ser	Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys

515

520

525

Cys Asp Tyr Pro Glu Ser Tyr Arg Gly Ser Pro Leu Lys Asp Phe His  
530 535 540 545

Met Ser Glu Leu Ser Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Gly  
550 555 560

Ala Thr Met Leu Val Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr  
565 570 575

Leu Asp Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr  
580 585 590

Arg Arg Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu  
595 600 605

Gln Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Ala Trp Val  
610 615 620 625

Lys Ser Glu Leu Val Pro Tyr Leu Glu Lys Glu Asp Ile Gln Ile Cys  
630 635 640

Leu His Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile  
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Ile Asn Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro  
660 665 670

Asn Phe Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His  
675 680 685

His Asn Leu Phe His Glu Gly Ser Asn Asn Leu Ile Leu Ile Leu Leu  
690 695 700 705

Glu Pro Ile Pro Gln Asn Ser Ile Pro Asn Lys Tyr His Lys Leu Lys  
710 715 720

Ala Leu Met Thr Gln Arg Thr Tyr Leu Gln Trp Pro Lys Glu Lys Ser  
725 730 735

Lys Arg Gly Leu Phe Trp Ala Asn Ile Arg Ala Ala Phe Asn Met Lys  
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&lt;212&gt; DNA

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Homo sapiens

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Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro  
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Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr  
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Gln	Ala	Leu	Glu	Val	Ala	Pro	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu		
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Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn		
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gac	ctc	tat	ctg	cac	ttc	ttc	caa	ggc	ctg	agc	ggg	ttg	atc	tgg	ctg	1968
Asp	Leu	Tyr	Leu	His	Phe	Phe	Gln	Gly	Leu	Ser	Gly	Leu	Ile	Trp	Leu	
		595					600					605				
gac	ttg	tcc	cag	aac	cgc	ctg	cac	acc	ctc	ctg	ccc	caa	acc	ctg	cgc	2016
Asp	Leu	Ser	Gln	Asn	Arg	Leu	His	Thr	Leu	Leu	Pro	Gln	Thr	Leu	Arg	
	610					615					620					
aac	ctc	ccc	aag	agc	cta	cag	gtg	ctg	cgt	ctc	cgt	gac	aat	tac	ctg	2064
Asn	Leu	Pro	Lys	Ser	Leu	Gln	Val	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	
625					630				635						640	
gcc	ctc	ttt	aag	tgg	tgg	agc	ctc	cac	ttc	ctg	ccc	aaa	ctg	gaa	gtc	2112
Ala	Phe	Phe	Lys	Trp	Trp	Ser	Leu	His	Phe	Leu	Pro	Lys	Leu	Glu	Val	
				645					650					655		
ctc	gac	ctg	gca	gga	aac	cag	ctg	aag	gcc	ctg	acc	aat	ggc	agc	ctg	2160
Leu	Asp	Leu	Ala	Gly	Asn	Gln	Leu	Lys	Ala	Leu	Thr	Asn	Gly	Ser	Leu	
			660					665					670			
cct	gct	ggc	acc	cgg	ctc	cgg	agg	ctg	gat	gtc	agc	tgc	aac	agc	atc	2208
Pro	Ala	Gly	Thr	Arg	Leu	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	Ile		
		675				680					685					
agc	ttc	gtg	gcc	ccc	ggc	ttc	ttt	tcc	aag	gcc	aag	gag	ctg	cga	gag	2256
Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	Glu	
	690					695					700					
ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	aca	gtg	gac	cac	tcc	tgg	ttt	2304
Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	Thr	Val	Asp	His	Ser	Trp	Phe	
705					710					715					720	
ggg	ccc	ctg	gcg	agt	gcc	ctg	caa	ata	cta	gat	gta	agc	gcc	aac	cct	2352
Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	
				725					730					735		
ctg	cac	tgc	gca	tgt	ggg	gcg	gcc	ttt	atg	gac	ttc	ctg	ctg	gag	gtg	2400
Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Glu	Glu	Val	
			740					745					750			
cag	gct	gcc	gtg	ccc	ggg	ctg	ccc	agc	cgg	gtg	aag	tgt	ggc	agt	ccg	2448

Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	Pro	
		755					760					765				
ggc	cag	ctc	cag	ggc	ctc	agc	atc	ttt	gca	cag	gac	ctg	cgc	ctc	tgc	2496
Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys	
		770				775					780					
ctg	gat	gag	gcc	ctc	tcc	tgg	gac	tgt	ttc	gcc	ctc	tgc	ctg	ctg	gct	2544
Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	Ala	
		785			790				795						800	
gtg	gct	ctg	ggc	ctg	ggt	gtg	ccc	atg	ctg	cat	cac	ctc	tgt	ggc	tgg	2592
Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp	
				805					810					815		
gac	ctc	tgg	tac	tgc	ttc	cac	ctg	tgc	ctg	gcc	tgg	ctt	ccc	tgg	cgg	2640
Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	Arg	
			820					825					830			
ggg	cgg	caa	agt	ggg	cga	gat	gag	gat	gcc	ctg	ccc	tac	gat	gcc	ttc	2688
Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe	
		835					840					845				
gtg	gtc	ttc	gac	aaa	acg	cag	agc	gca	gtg	gca	gac	tgg	gtg	tac	aac	2736
Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn	
		850				855					860					
gag	ctt	cgg	ggg	cag	ctg	gag	gag	tgc	cgt	ggg	cgc	tgg	gca	ctc	cgc	2784
Glu	Leu	Arg	Gly	Gln	Leu	Glu	Glu	Cys	Arg	Gly	Arg	Trp	Ala	Leu	Arg	
		865			870				875						880	
ctg	tgc	ctg	gag	gaa	cgc	gac	tgg	ctg	cct	ggc	aaa	acc	ctc	ttt	gag	2832
Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Lys	Thr	Leu	Phe	Glu	
				885					890					895		
aac	ctg	tgg	gcc	tgc	gtc	tat	ggc	agc	cgc	aag	acg	ctg	ttt	gtg	ctg	2880
Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu	
			900					905					910			
gcc	cac	acg	gac	cgg	gtc	agt	ggt	ctc	ttg	cgc	gcc	agc	ttc	ctg	ctg	2928
Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	Leu	
		915					920					925				
gcc	cag	cag	cgc	ctg	ctg	gag	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	2976
Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	
		930				935					940					
atc	ctg	agc	cct	gac	ggc	cgc	cgc	tcc	cgc	tat	gtg	cgg	ctg	cgc	cag	3024
Ile	Leu	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln	
		945			950					955					960	
cgc	ctc	tgc	cgc	cag	agt	gtc	ctc	ctc	tgg	ccc	cac	cag	ccc	agt	ggt	3072
Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Leu	Trp	Pro	His	Gln	Pro	Ser	Gly	
				965					970					975		

jag	cgc	agc	ttc	tgg	gcc	cag	ctg	ggc	atg	gcc	ctg	acc	agg	gac	aac	3120
fln	Arg	Ser	Phe	Trp	Ala	Gln	Leu	Gly	Met	Ala	Leu	Thr	Arg	Asp	Asn	
			980					985					990			

jac	cac	ttc	tat	aac	cgg	aac	ttc	tgc	cag	gga	ccc	acg	gcc	gaa	tag	3168
lis	His	Phe	Tyr	Asn	Arg	Asn	Phe	Cys	Gln	Gly	Pro	Thr	Ala	Glu		
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<211> 1055

<212> PRT

<213> Unknown

<400> 43

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		-30					-25					-20				

Pro	Leu	Ser	Leu	Leu	Val	Gln	Ala	Ile	Met	Leu	Ala	Met	Thr	Leu	Ala	
	-15				-10						-5				-1	

Leu	Gly	Thr	Leu	Pro	Ala	Phe	Leu	Pro	Cys	Glu	Leu	Gln	Pro	His	Gly	
1			5					10					15			

Leu	Val	Asn	Cys	Asn	Trp	Leu	Phe	Leu	Lys	Ser	Val	Pro	His	Phe	Ser	
		20						25					30			

Met	Ala	Ala	Pro	Arg	Gly	Asn	Val	Thr	Ser	Leu	Ser	Leu	Ser	Ser	Asn	
	35					40						45				

Arg	Ile	His	His	Leu	His	Asp	Ser	Asp	Phe	Ala	His	Leu	Pro	Ser	Leu	
	50					55					60					

Arg	His	Leu	Asn	Leu	Lys	Trp	Asn	Cys	Pro	Pro	Val	Gly	Leu	Ser	Pro	
65				70					75					80		

Met	His	Phe	Pro	Cys	His	Met	Thr	Ile	Glu	Pro	Ser	Thr	Phe	Leu	Ala	
			85					90					95			

Val	Pro	Thr	Leu	Glu	Glu	Leu	Asn	Leu	Ser	Tyr	Asn	Asn	Ile	Met	Thr	
		100					105					110				

Val	Pro	Ala	Leu	Pro	Lys	Ser	Leu	Ile	Ser	Leu	Ser	Leu	Ser	His	Thr	
	115				120							125				

Asn	Ile	Leu	Met	Leu	Asp	Ser	Ala	Ser	Leu	Ala	Gly	Leu	His	Ala	Leu	
	130				135						140					

Arg	Phe	Leu	Phe	Met	Asp	Gly	Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Arg	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

145		150		155		160
Gln Ala Leu Glu Val Ala Pro Gly Ala Leu Leu Gly Leu Gly Asn Leu						
	165			170		175
Thr His Leu Ser Leu Lys Tyr Asn Asn Leu Thr Val Val Pro Arg Asn						
	180		185			190
Leu Pro Ser Ser Leu Glu Tyr Leu Leu Leu Ser Tyr Asn Arg Ile Val						
	195		200			205
Lys Leu Ala Pro Glu Asp Leu Ala Asn Leu Thr Ala Leu Arg Val Leu						
	210		215			220
Asp Val Gly Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys						
	225		230		235	240
Met Glu Cys Pro Arg His Phe Pro Gln Leu His Pro Asp Thr Phe Ser						
		245		250		255
His Leu Ser Arg Leu Glu Gly Leu Val Leu Lys Asp Ser Ser Leu Ser						
		260		265		270
Trp Leu Asn Ala Ser Trp Phe Arg Gly Leu Gly Asn Leu Arg Val Leu						
		275		280		285
Asp Leu Ser Glu Asn Phe Leu Tyr Lys Cys Ile Thr Lys Thr Lys Ala						
	290		295		300	
Phe Gln Gly Leu Thr Gln Leu Arg Lys Leu Asn Leu Ser Phe Asn Tyr						
	305		310		315	320
Gln Lys Arg Val Ser Phe Ala His Leu Ser Leu Ala Pro Ser Phe Gly						
		325		330		335
Ser Leu Val Ala Leu Lys Glu Leu Asp Met His Gly Ile Phe Phe Arg						
		340		345		350
Ser Leu Asp Glu Thr Thr Leu Arg Pro Leu Ala Arg Leu Pro Met Leu						
		355		360		365
Gln Thr Leu Arg Leu Gln Met Asn Phe Ile Asn Gln Ala Gln Leu Gly						
		370		375		380
Ile Phe Arg Ala Phe Pro Gly Leu Arg Tyr Val Asp Leu Ser Asp Asn						
	385		390		395	400
Arg Ile Ser Gly Ala Ser Glu Leu Thr Ala Thr Met Gly Glu Ala Asp						
		405		410		415
Gly Gly Glu Lys Val Trp Leu Gln Pro Gly Asp Leu Ala Pro Ala Pro						
		420		425		430
Val Asp Thr Pro Ser Ser Glu Asp Phe Arg Pro Asn Cys Ser Thr Leu						

435

440

445

Asn Phe Thr Leu Asp Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro  
450 455 460

Glu Met Phe Ala Gln Leu Ser His Leu Gln Cys Leu Arg Leu Ser His  
465 470 475 480

Asn Cys Ile Ser Gln Ala Val Asn Gly Ser Gln Phe Leu Pro Leu Thr  
485 490 495

Gly Leu Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His  
500 505 510

Glu His Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser  
515 520 525

Tyr Asn Ser Gln Pro Phe Gly Met Gln Gly Val Gly His Asn Phe Ser  
530 535 540

Phe Val Ala His Leu Arg Thr Leu Arg His Leu Ser Leu Ala His Asn  
545 550 555 560

Asn Ile His Ser Gln Val Ser Gln Gln Leu Cys Ser Thr Ser Leu Arg  
565 570 575

Ala Leu Asp Phe Ser Gly Asn Ala Leu Gly His Met Trp Ala Glu Gly  
580 585 590

Asp Leu Tyr Leu His Phe Phe Gln Gly Leu Ser Gly Leu Ile Trp Leu  
595 600 605

Asp Leu Ser Gln Asn Arg Leu His Thr Leu Leu Pro Gln Thr Leu Arg  
610 615 620

Asn Leu Pro Lys Ser Leu Gln Val Leu Arg Leu Arg Asp Asn Tyr Leu  
625 630 635 640

Ala Phe Phe Lys Trp Trp Ser Leu His Phe Leu Pro Lys Leu Glu Val  
645 650 655

Leu Asp Leu Ala Gly Asn Gln Leu Lys Ala Leu Thr Asn Gly Ser Leu  
660 665 670

Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser Ile  
675 680 685

Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg Glu  
690 695 700

Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp Phe  
705 710 715 720

Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	725	730	735
Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	740	745	750
Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	Pro	755	760	765
Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys	770	775	780
Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	Ala	785	790	800
Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp	805	810	815
Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	Arg	820	825	830
Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe	835	840	845
Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn	850	855	860
Glu	Leu	Arg	Gly	Gln	Leu	Glu	Glu	Cys	Arg	Gly	Arg	Trp	Ala	Leu	Arg	865	870	875
Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Lys	Thr	Leu	Phe	Glu	885	890	895
Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu	900	905	910
Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	Leu	915	920	925
Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	930	935	940
Ile	Leu	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln	945	950	955
Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Leu	Trp	Pro	His	Gln	Pro	Ser	Gly	965	970	975
Gln	Arg	Ser	Phe	Trp	Ala	Gln	Leu	Gly	Met	Ala	Leu	Thr	Arg	Asp	Asn	980	985	990
His	His	Phe	Tyr	Asn	Arg	Asn	Phe	Cys	Gln	Gly	Pro	Thr	Ala	Glu		995	1000	1005

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 <211> 2289  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:rodent; surmised  
 Mus musculus

<220>  
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 <222> (1)..(2079)

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 1 5 10 15  
 ctg gca agt tcc ttt aag aac ctg gtg tca ctg cag gag ctg aac atg 96  
 Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu Leu Asn Met  
 20 25 30  
 aacggc atc ttc ttc cgc ttg ctc aac aag tac acg ctc aga tgg ctg 144  
 AsnGly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu  
 35 40 45  
 gccgat ctg ccc aaa ctc cac act ctg cat ctt caa atg aac ttc atc 192  
 Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile  
 50 55 60  
 aac-cag gca cag ctc agc atc ttt ggt acc ttc cga gcc ctt cgc ttt 240  
 AsnGln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe  
 65 70 75 80  
 -gtg gac ttg tca gac aat cgc atc agt ggg cct tca acg ctg tca gaa 288  
 Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu  
 85 90 95  
 gcc acc cct gaa gag gca gat gat gca gag cag gag gag ctg ttg tct 336  
 Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser  
 100 105 110  
 gcg gat cct cac cca gct ccg ctg agc acc cct gct tct aag aac ttc 384  
 Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe  
 115 120 125  
 atg gac agg tgt aag aac ttc aag ttc aac atg gac ctg tct cgg aac 432  
 Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn  
 130 135 140  
 aac ctg gtg act atc aca gca gag atg ttt gta aat ctc tca cgc ctc 480  
 Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu



145		150		155		160	
cag tgt ctt agc ctg agc cac aac tca att gca cag gct gtc aat ggc 528							
Gln Cys Leu Ser 165				Ile Ala Gln Ala Val Asn Gly 175			
tct cag ttc ctg ccg ctg acc ggt ctg cag gtg cta gac ctg tcc cac 576							
Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu Ser His 180				185		190	
aat aag ctg gac ctc tac cac gag cac tca ttc acg gag cta cca cga 624							
Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr 200				205		210	
ctg gag gcc ctg gac ctc agc tac aac agc cag ccc ttt agc atg aag 672							
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Lys 210				215		220	
ggg ata ggc cac aat ttc agt ttt gtg acc cat ctg tcc atg cta cag 720							
Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser Met Leu Gln 225				230		235	240
agg ctt agc ctg gca cac aat gac att cat acc cgt gtg tcc tca cat 768							
Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val Ser Ser His 245				250		255	
ctc aac agc aac tca gtg agg ttt ctt gac ttc agc ggc aac ggt atg 816							
Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly Asn Gly Met 260				265		270	
ggc cgc atg tgg gat gag ggg ggc ctt tat ctc cat ttc ttc caa ggc 864							
Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe Phe Gln Gly 275				280		285	
ctg agt ggc gtg ctg aag ctg gac ctg tct caa aat aac ctg cat atc 912							
Leu Ser Gly Val Leu Lys Leu Asp Leu Ser Gln Asn Asn Leu His Ile 290				295		300	
ctc cgg ccc cag aac ctt gac aac ctc ccc aag agc ctg aag ctg ctg 960							
Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu Lys Leu Leu 305				310		315	320
agc ctc cga gac aac tac cta tct ttc ttt aac tgg acc agt ctg tcc 1008							
Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr Ser Ser Ser 325				330		335	
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Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn Gln Leu Lys 340				345		350	
gcc ctg acc aat ggc acc ctg cct aat ggc acc ctc ctc cag aaa ctc 1104							
Ala Leu Thr 355				360		365	

gat Asp	gtc Val	agt Ser	agc Ser	aac Asn	agt Ser	atc Ile	gtc Val	tct Ser	gtg Val	gcc Ala	ccc Pro	ggc Gly	ttc Phe	ttt Phe	tcc Ser	1152
370						375					380					
aag Lys	gcc Ala	aag Lys	gag Glu	ctg Leu	cga Arg	gag Glu	ctc Leu	aac Asn	ctt Leu	agc Ser	gcc Ala	aac Asn	gcc Ala	ctc Leu	aag Lys	1200
385					390					395					400	
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				405					410						415	
cta Leu	gac Asp	gtg Val	aga Arg	agc Ser	aac Asn	cct Pro	ctg Leu	cac His	tgt Cys	gcc Ala	tgt Cys	ggg Gly	gca Ala	gcc Ala	ttc Phe	1296
				420					425					430		
gta Val	gac Asp	tta Leu	ctg Leu	ttg Leu	gag Glu	gtg Val	cag Gln	acc Thr	aag Lys	gtg Val	cct Pro	ggc Gly	ctg Leu	gct Ala	aat Asn	1344
							440									
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465					470					475					480	
ttt Phe	ggc Gly	ctt Leu	tca Ser	ctc Leu	ttg Leu	gct Ala	gtg Val	gcc Ala	gtg Val	ggc Gly	atg Met	gtg Val	gtg Val	cct Pro	ata Ile	1488
				485					490						495	
ctg Leu	cac His	cat His	ctc Leu	tgc Cys	ggc Gly	tgg Trp	gac Asp	gtc Val	tgg Trp	tac Tyr	tgt Cys	ttt Phe	cat His	ctg Leu	tgc Cys	1536
				500				505					510			
ctg Leu	gca Ala	tgg Trp	cta Leu	cct Pro	ttg Leu	cta Leu	gcc Ala	cgc Arg	agc Ser	cga Arg	cgc Arg	agc Ser	gcc Ala	caa Gln	act Thr	1584
				515			520					525				
ctc Leu	cct Pro	tat Tyr	gat Asp	gcc Ala	ttc Phe	gtg Val	gtg Val	ttc Phe	gat Asp	aag Lys	gca Ala	cag Gln	agc Ser	gca Ala	gtt Val	1632
		530				535					540					
gcc Ala	gac Asp	tgg Trp	gtg Val	tat Tyr	aac Asn	gag Glu	ctg Leu	cgg Arg	gtg Val	cgg Arg	ctg Leu	gag Glu	gag Glu	cgg Arg	cgc Arg	1680
545					550				555						560	
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 20 25 30  
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 35 40 45  
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50

55

60

Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe  
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Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu  
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Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser  
100 105 110

Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe  
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Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn  
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Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu  
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Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala Val Asn Gly  
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Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu Ser His  
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Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Lys  
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APPLICATION NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTY. DOCKET NO./TITLE
09/728,540	11/28/2000	Gerard T. Hardiman	DX0724XK

CONFIRMATION NO. 4490

CORRECTION COVER LETTER



\*0C000000006158481\*

28008  
DNAX RESEARCH INSTITUTE  
LEGAL DEPARTMENT  
901 CALIFORNIA AVENUE  
PALO ALTO, CA 94304

Date Mailed: 06/07/2001

## COVER LETTER FOR CORRECTION OF PREVIOUS NOTICE

The Notice mailed on 02/08/2001 was sent in error and is hereby withdrawn. A corrected Notice is enclosed.  
The time period for reply runs from the mail date of the corrected Notice. We apologize for any  
inconvenience this caused.

2001-07-06 10:05:01

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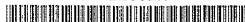
APPLICATION NUMBER	FILING RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/728,540	11/28/2000	Gerard T. Hardiman	DX0724XK

CONFIRMATION NO. 4490

28008

DNAX RESEARCH INSTITUTE  
LEGAL DEPARTMENT  
901 CALIFORNIA AVENUE  
PALO ALTO, CA 94304

FORMALITIES LETTER



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### NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given TWO MONTHS FROM THE DATE OF THIS NOTICE within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- This application does not contain a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). Applicant must provide such statement. If the effective filing date is on or after September 8, 2000, see the final rulemaking notice published in the Federal Register at 65 FR 54604 (September 8, 2000) and 1238 OG 145 (September 19, 2000).
- A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e). If the effective filing date is on or after September 8, 2000, see the final rulemaking notice published in the Federal Register at 65 FR 54604 (September 8, 2000) and 1238 OG 145 (September 19, 2000). Applicant must provide an initial computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). If applicant desires the sequence listing in the instant application to be identical with that of another application on file in the U.S. Patent and Trademark Office, such request in accordance with 37 CFR 1.821(e) may be submitted in lieu of a new CRF.

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